



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 153366

TO: Andrew D Kosar
Location: rem/3c04/3c18
Art Unit: 1654
Wednesday, May 18, 2005

Case Serial Number: 10/731921

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Kosar,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 09:59:56 ; Search time 58 Seconds
(without alignments)
35.316 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	30	2 Q91HB7	Q91hb7 tt virus. o
2	23	100.0	31	2 Q8VJ21	Q8vj21 mycobacteri
3	23	100.0	34	2 O06618	O06618 mycobacteri
4	23	100.0	34	2 Q7T2W6	Q7t2w6 mycobacteri
5	23	100.0	35	2 Q679Y6	Q679y6 pan troglod
6	23	100.0	36	2 Q679Y8	Q679y8 pan troglod
7	23	100.0	39	2 Q9UEU6	Q9ueu6 homo sapien
8	23	100.0	43	1 IM9A.RAT	Q9wv97 rattus norv
9	23	100.0	52	2 Q6M2F9	Q6m2f9 homo sapien
10	23	100.0	59	2 Q71V32	Q71v32 rattus norv
11	23	100.0	61	2 Q54820	Q54820 streptomyce
12	23	100.0	62	2 Q6BWM8	Q6bwm8 debaryomyce
13	23	100.0	63	2 Q8U521	Q8u521 agrobacteri
14	23	100.0	65	2 Q8VMW9	Q8vmw9 anabaena sp
15	23	100.0	67	2 Q9K880	Q9k880 bacillus ha
16	23	100.0	72	2 Q7UWU3	Q7uwu3 rhodospirell
17	23	100.0	73	2 Q7PF50	Q7pf50 anopheles g
18	23	100.0	73	2 Q6A863	Q6a863 propionibac
19	23	100.0	73	2 Q80W36	Q80w36 mus musculu
20	23	100.0	74	2 Q7V8P7	Q7v8p7 prochloroco
21	23	100.0	75	2 Q8DH17	Q8dh17 synchococc
22	23	100.0	76	2 Q6TLI2	Q6tli2 streptomyce
23	23	100.0	77	2 Q7R5L8	Q7r5l8 giardia lam
24	23	100.0	81	2 Q6ESF6	Q6esf6 oryza sativ
25	23	100.0	81	2 Q8P835	Q8p835 xanthomonas
26	23	100.0	81	2 Q72CR2	Q72cr2 desulfovibr
27	23	100.0	82	2 Q96Q33	Q96q33 homo sapien
28	23	100.0	82	2 Q9X5W4	Q9x5w4 rhodobacter
29	23	100.0	85	2 Q86T70	Q86t70 homo sapien
30	23	100.0	85	2 Q8S0W2	Q8s0w2 oryza sativ
31	23	100.0	86	2 Q856X1	Q856x1 mycobacteri

32	23	100.0	87	2 Q8WZ93	Q8wz93 homo sapien
33	23	100.0	87	2 Q7U442	Q7u442 synchococc
34	23	100.0	88	1 GVPB.BACME	G68677 bacillus me
35	23	100.0	89	1 IM9A_HUMAN	Q9y517 homo sapien
36	23	100.0	89	1 IM9A_MOUSE	Q9w938 mus musculu
37	23	100.0	89	2 Q68V99	Q68v99 uncultured
38	23	100.0	89	2 Q9DSU8	Q9deu8 ascovirus d
39	23	100.0	90	1 HYPC.ECOLI	P24191 escherichia
40	23	100.0	90	2 Q8XG01	Q8xg01 salmonella
41	23	100.0	90	2 Q7CPX9	Q7cpx9 salmonella
42	23	100.0	90	2 Q7R0F6	Q7r0f6 bordetella
43	23	100.0	90	2 Q7WID7	Q7wid7 bordetella
44	23	100.0	90	2 Q7WPD4	Q7wpd4 bordetella
45	23	100.0	91	2 Q8YRZ8	Q8yrz8 anabaena sp
46	23	100.0	92	2 Q84VP6	Q84vp6 arabidopsis
47	23	100.0	94	2 Q91UP6	Q91up6 plasmiid' pbb
48	23	100.0	95	2 Q8SA29	Q8sa29 oryza sativ
49	23	100.0	96	2 Q9F6C4	Q9f6c4 propionibac
50	23	100.0	98	2 Q9YCI1	Q9yci1 aeropyrum p
51	23	100.0	98	2 Q7QUD9	Q7qud9 giardia lam
52	23	100.0	99	2 Q6QOC8	Q6qoc8 human immun
53	23	100.0	99	2 Q9Q2H7	Q9q2h7 human immun
54	23	100.0	100	2 Q9QDC9	Q9qdc9 chimpanzee
55	23	100.0	101	2 Q7PJ39	Q7pj39 anopheles g
56	23	100.0	101	2 Q7G4Y8	Q7g4y8 oryza sativ
57	23	100.0	101	2 Q8Q57	Q8q57 pseudomonas
58	23	100.0	101	2 Q9RWS5	Q9rws5 deinococcus
59	23	100.0	101	2 Q8UEN1	Q8uen1 agrobacteri
60	23	100.0	102	2 Q79F64	Q79f64 anabaena va
61	23	100.0	102	2 Q44560	Q44560 anabaena sp
62	23	100.0	102	2 Q8CAG4	Q8cag4 mus musculu
63	23	100.0	103	2 Q6Z289	Q6z289 oryza sativ
64	23	100.0	103	2 Q934X9	Q934x9 salmonella
65	23	100.0	103	2 Q6LV85	Q6lv85 photobacter
66	23	100.0	103	2 Q9Q2P0	Q9q2p0 human herpe
67	23	100.0	104	1 VPR.HV2ST	F20884 human immun
68	23	100.0	105	1 VPR.HV2SB	P12455 human immun
69	23	100.0	106	2 Q9FTT2	Q9ftt2 oryza sativ
70	23	100.0	106	2 Q9ST59	Q9st59 arabidopsis
71	23	100.0	106	2 Q92NZ1	Q92nz1 rhizobium m
72	23	100.0	107	2 Q7R3Y4	Q7r3y4 giardia lam
73	23	100.0	108	2 Q820P4	Q820p4 nitrosomona
74	23	100.0	109	2 Q9YDJ3	Q9ydj3 aeropyrum p
75	23	100.0	109	2 Q8S5J0	Q8s5j0 oryza sativ
76	23	100.0	109	2 Q30535	Q30535 pseudomonas
77	23	100.0	109	2 Q91328	Q91328 pseudomonas
78	23	100.0	109	2 Q8CAU8	Q8cau8 mus musculu
79	23	100.0	111	2 Q6IM28	Q6im28 drosophila
80	23	100.0	111	2 Q69X79	Q69x79 oryza sativ
81	23	100.0	111	2 Q8KL09	Q8kl09 rhizobium e
82	23	100.0	112	2 Q8L4D1	Q8l4d1 oryza sativ
83	23	100.0	112	2 Q6H5I3	Q6h5i3 oryza sativ
84	23	100.0	113	2 Q7Z2D7	Q7z2d7 homo sapien
85	23	100.0	113	2 Q8PIK5	Q8pik5 xanthomonas
86	23	100.0	115	2 Q783I5	Q783i5 neorospira
87	23	100.0	115	2 Q9T220	Q9t220 caenorhabdi
88	23	100.0	115	2 Q8Z6T2	Q8z6t2 salmonella
89	23	100.0	116	2 Q9N0B1	Q9n0b1 macaca fasc
90	23	100.0	117	2 Q745T3	Q745t3 thermus the
91	23	100.0	118	2 Q69JY2	Q69jy2 oryza sativ
92	23	100.0	119	2 Q8NG30	Q8ng30 homo sapien
93	23	100.0	119	2 Q8S438	Q8s438 sorghum bic
94	23	100.0	120	2 Q6EIQ5	Q6eiq5 bos taurus
95	23	100.0	121	2 Q6BSN1	Q6bsn1 debaryomyce
96	23	100.0	121	2 Q7XMS8	Q7xm8 oryza sativ
97	23	100.0	122	2 Q9RVZ1	Q9rvz1 deinococcus
98	23	100.0	123	2 Q73YI4	Q73yi4 mycobacteri
99	23	100.0	124	2 Q6SF14	Q6sf14 bacillus li
100	23	100.0	124	2 Q8G1S0	Q8g1s0 brucella eu
101	23	100.0	124	2 Q8EM12	Q8em12 mus musculu
102	23	100.0	125	2 Q95UI4	Q95ui4 drosophila
103	23	100.0	126	2 Q86WR6	Q86wr6 homo sapien
104	23	100.0	126	2 Q7PHJ7	Q7phj7 anopheles g

105	23	100.0	126	2	Q92241	Q92441 rhizobium m	178	23	100.0	149	2	Q55148	Q55148 synechocyst
106	23	100.0	126	2	Q9K415	Q9K415 streptomyc	179	23	100.0	149	2	Q8Q5E0	Q8Q5E0 chimpanzee
107	23	100.0	127	2	Q75Gw7	Q75Gw7 oryza sativ	180	23	100.0	150	2	Q8UIY6	Q8UIY6 agrobacteri
108	23	100.0	127	2	Q46488	Q46488 leifsonia x	181	23	100.0	150	2	Q8XXF1	Q8XXF1 raietonia s
109	23	100.0	128	2	Q716J3	Q716J3 mycobacteri	182	23	100.0	150	2	Q8Q4Y1	Q8Q4Y1 chimpanzee
110	23	100.0	128	2	Q69WY6	Q69WY6 oryza sativ	183	23	100.0	151	2	P71854	P71854 mycobacteri
111	23	100.0	128	2	Q7CRK6	Q7CRK6 agrobacteri	184	23	100.0	151	2	Q7TW86	Q7TW86 aeropyrum p
112	23	100.0	128	2	Q881V3	Q881V3 pseudomonas	185	23	100.0	152	2	Q9YFZ5	Q9YFZ5 aeropyrum p
113	23	100.0	129	2	Q9BZX3	Q9BZX3 homo sapien	186	23	100.0	152	2	Q9N1U1	Q9N1U1 tupaiia glis
114	23	100.0	129	2	Q7AX55	Q7AX55 neisseria m	187	23	100.0	152	2	Q9R6K8	Q9R6K8 agrobacteri
115	23	100.0	129	2	P95144	P95144 mycobacteri	188	23	100.0	153	2	Q87ZA9	Q87ZA9 pseudomonas
116	23	100.0	129	2	Q7TZE5	Q7TZE5 mycobacteri	189	23	100.0	153	2	Q9HU57	Q9HU57 pseudomonas
117	23	100.0	129	2	Q9CB30	Q9CB30 mycobacteri	190	23	100.0	154	2	Q96SK9	Q96SK9 homo sapien
118	23	100.0	129	2	Q9JON5	Q9JON5 neisseria m	191	23	100.0	154	2	Q7QUAO	Q7QUAO giardia lam
119	23	100.0	131	2	Q8H5M1	Q8H5M1 oryza sativ	192	23	100.0	154	2	Q848I8	Q848I8 pseudomonas
120	23	100.0	131	2	Q683Q0	Q683Q0 uncultured	193	23	100.0	154	2	Q8PF84	Q8PF84 xanthomonas
121	23	100.0	132	2	Q8BQ19	Q8BQ19 halobacteri	194	23	100.0	155	1	PA2X_HUMAN	PA2X_HUMAN
122	23	100.0	132	2	Q8NHP21	Q8NHP21 homo sapien	195	23	100.0	155	2	Q6EPL5	Q6EPL5 oryza sativ
123	23	100.0	132	2	Q8N7H7	Q8N7H7 rhizobium m	196	23	100.0	155	2	Q6ZG41	Q6ZG41 oryza sativ
124	23	100.0	132	2	Q52889	Q52889 rhizobium m	197	23	100.0	155	2	Q830F9	Q830F9 enterococcu
125	23	100.0	132	2	Q9FCX1	Q9FCX1 erwinia amy	198	23	100.0	157	2	Q7SBW3	Q7SBW3 neurospora
126	23	100.0	132	2	Q73UX3	Q73UX3 mycobacteri	199	23	100.0	157	2	Q6ZKY5	Q6ZKY5 oryza sativ
127	23	100.0	132	2	Q7UKC4	Q7UKC4 rhodopirell	200	23	100.0	157	2	Q9RXG1	Q9RXG1 deinococcus
128	23	100.0	132	2	Q8BQ19	Q8BQ19 mus musculus	201	23	100.0	157	2	Q8U631	Q8U631 agrobacteri
129	23	100.0	133	2	Q7X2Y4	Q7X2Y4 uncultured	202	23	100.0	157	2	Q9JJ33	Q9JJ33 mus musculus
130	23	100.0	133	2	Q9ZEP9	Q9ZEP9 pseudomonas	203	23	100.0	159	2	Q6ES35	Q6ES35 oryza sativ
131	23	100.0	134	2	Q8N2U4	Q8N2U4 homo sapien	204	23	100.0	159	2	Q88DX0	Q88DX0 pseudomonas
132	23	100.0	134	2	Q54682	Q54682 lactococcus	205	23	100.0	160	2	Q8H830	Q8H830 oryza sativ
133	23	100.0	135	1	Y274_BUCAI	Y274_BUCAI	206	23	100.0	160	2	Q910Y0	Q910Y0 streptomyc
134	23	100.0	135	2	Q81Y04	Q81Y04 buchnera ap	207	23	100.0	161	2	Q85679	Q85679 micromonos
135	23	100.0	135	2	Q624C7	Q624C7 oryza sativ	208	23	100.0	161	2	Q8UBC4	Q8UBC4 agrobacteri
136	23	100.0	135	2	Q7NY82	Q7NY82 chromobacte	209	23	100.0	162	2	Q26526	Q26526 methanobact
137	23	100.0	135	2	Q8CF47	Q8CF47 mus musculus	210	23	100.0	162	2	Q8N2B5	Q8N2B5 homo sapien
138	23	100.0	137	2	Q95UI3	Q95UI3 drosophila	211	23	100.0	162	2	Q6ZTGS	Q6ZTGS macaca mula
139	23	100.0	137	2	Q82N20	Q82N20 streptomyc	212	23	100.0	162	2	Q8HX38	Q8HX38 micromonos
140	23	100.0	138	1	PA2_BOTIN	PA2_BOTIN	213	23	100.0	162	2	Q85680	Q85680 xanthomonas
141	23	100.0	138	2	Q9YCZ0	Q9YCZ0 aeropyrum p	214	23	100.0	162	2	Q8PFY1	Q8PFY1 xanthomonas
142	23	100.0	138	2	Q84949	Q84949 salmonella	215	23	100.0	162	2	Q6A5J9	Q6A5J9 propionibac
143	23	100.0	138	2	Q8Z6L8	Q8Z6L8 salmonella	216	23	100.0	162	2	Q9WU17	Q9WU17 mesocricetu
144	23	100.0	139	2	Q7RUE1	Q7RUE1 neurospora	217	23	100.0	163	2	Q6KAI1	Q6KAI1 oryza sativ
145	23	100.0	139	2	Q94221	Q94221 caenorhabdi	218	23	100.0	163	2	Q52169	Q52169 salmonella
146	23	100.0	139	2	Q6Z637	Q6Z637 oryza sativ	219	23	100.0	164	2	Q8BS64	Q8BS64 mus musculus
147	23	100.0	139	2	Q84NW4	Q84NW4 oryza sativ	220	23	100.0	165	2	Q9HHG9	Q9HHG9 halobacteri
148	23	100.0	139	2	Q8YGS2	Q8YGS2 brucella me	221	23	100.0	165	2	Q6NT23	Q6NT23 homo sapien
149	23	100.0	140	1	YK24_PSEAE	YK24_PSEAE	222	23	100.0	165	2	Q84ZG0	Q84ZG0 oryza sativ
150	23	100.0	140	2	Q8GZ25	Q8GZ25 pseudomonas	223	23	100.0	165	2	Q9RJW7	Q9RJW7 arabisidopsis
151	23	100.0	140	2	Q7NF01	Q7NF01 oryza sativ	224	23	100.0	165	2	Q9M2X2	Q9M2X2 arabisidopsis
152	23	100.0	140	2	Q87W37	Q87W37 pseudomonas	225	23	100.0	166	1	ALLA_AGR5	ALLA_AGR5
153	23	100.0	140	2	Q6D4S6	Q6D4S6 erwinia car	226	23	100.0	166	2	Q7QPP7	Q7QPP7 giardia lam
154	23	100.0	140	2	Q87483	Q87483 chimpanzee	227	23	100.0	166	2	Q23694	Q23694 arabisidopsis
155	23	100.0	141	2	Q9MXT1	Q9MXT1 macaca mula	228	23	100.0	166	2	Q8KZ43	Q8KZ43 uncultured
156	23	100.0	141	2	Q7VYB1	Q7VYB1 bordetella	229	23	100.0	166	2	Q8PDL2	Q8PDL2 xanthomonas
157	23	100.0	141	2	Q7WJ76	Q7WJ76 bordetella	230	23	100.0	166	2	Q9DAB3	Q9DAB3 mus musculus
158	23	100.0	141	2	Q9RU64	Q9RU64 deinococcus	231	23	100.0	166	2	Q6INP4	Q6INP4 xenopus lae
159	23	100.0	143	2	Q741M5	Q741M5 mycobacteri	232	23	100.0	167	2	Q9VZ23	Q9VZ23 methanobact
160	23	100.0	143	2	Q9CZ27	Q9CZ27 mus musculus	233	23	100.0	167	2	Q985V9	Q985V9 rhizobium l
161	23	100.0	144	2	Q9HRN7	Q9HRN7 halobacteri	234	23	100.0	168	1	MOAC_DEIRA	MOAC_DEIRA
162	23	100.0	144	2	Q99K51	Q99K51 mus musculus	235	23	100.0	168	2	Q8S0M0	Q8S0M0 oryza sativ
163	23	100.0	145	2	Q9UVJ7	Q9UVJ7 aspergillus	236	23	100.0	168	2	Q8H4P3	Q8H4P3 oryza sativ
164	23	100.0	145	2	Q9H219	Q9H219 pseudomonas	237	23	100.0	168	2	Q7VJTM8	Q7VJTM8 helicobacte
165	23	100.0	146	2	Q9GU56	Q9GU56 heterodera	238	23	100.0	168	2	Q7VXK4	Q7VXK4 bordetella
166	23	100.0	146	2	Q97498	Q97498 oryctolagus	239	23	100.0	168	2	Q7W8Z3	Q7W8Z3 bordetella
167	23	100.0	146	2	Q745H4	Q745H4 mycobacteri	240	23	100.0	168	2	Q7WKD6	Q7WKD6 bordetella
168	23	100.0	146	2	Q88L05	Q88L05 pseudomonas	241	23	100.0	168	2	Q888Q4	Q888Q4 pseudomonas
169	23	100.0	147	2	Q70TE9	Q70TE9 drosophila	242	23	100.0	169	1	CF2A_MOUSE	CF2A_MOUSE
170	23	100.0	147	2	Q55533	Q55533 synechocyst	243	23	100.0	170	1	ALLI_RHIME	ALLI_RHIME
171	23	100.0	147	2	Q8BNP1	Q8BNP1 mus musculus	244	23	100.0	170	2	Q62JH1	Q62JH1 rhizobium m
172	23	100.0	148	2	Q9REU8	Q9REU8 pseudomonas	245	23	100.0	170	2	Q63T54	Q63T54 burkholderi
173	23	100.0	148	2	Q743S2	Q743S2 mycobacteri	246	23	100.0	171	2	Q9NPV6	Q9NPV6 homo sapien
174	23	100.0	148	2	Q9CH09	Q9CH09 lactococcus	247	23	100.0	171	2	Q9A4Q2	Q9A4Q2 caulobacter
175	23	100.0	149	2	Q8PU26	Q8PU26 methanobact	248	23	100.0	171	2	Q8C2X6	Q8C2X6 mus musculus
176	23	100.0	149	2	Q6IKD6	Q6IKD6 drosophila	249	23	100.0	172	2	Q8W2X4	Q8W2X4 oryza sativ
177	23	100.0	149	2	Q8GA35	Q8GA35 escherichia	250	23	100.0	172	2	Q6Q1W0	Q6Q1W0 chlamydomon

251	23	100.0	172	2	Q8CEI4	Q8cei4 mus musculus	324	23	100.0	195	2	O89172	O89172 rice grassy
252	23	100.0	174	2	Q9FLI1	Q9fli1 arabidopsis	325	23	100.0	195	2	Q91144	Q91144 rice grassy
253	23	100.0	176	2	Q7TUY0	Q7tuy0 prochloroco	326	23	100.0	195	2	Q91W24	Q91W24 cactus viru
254	23	100.0	176	2	Q87WA2	Q87wa2 pseudomonas	327	23	100.0	196	2	O8N931	O8N931 homo sapien
255	23	100.0	176	2	Q9KD61	Q9kd61 bacillus ha	328	23	100.0	196	2	Q8ILF1	Q8ilf1 drosophila
256	23	100.0	176	2	Q9RWDJ3	Q9rwj3 deinococcus	329	23	100.0	196	2	Q9HU79	Q9hu79 pseudomonas
257	23	100.0	177	1	Y254 PYRFU	Q8u441 pyrococcus	330	23	100.0	196	2	Q912F0	Q912f0 mus musculus
258	23	100.0	177	2	Q93311	Q93311 caenorhabdi	331	23	100.0	197	1	ATKC CAUCR	Q9a7x6 caulobacter
259	23	100.0	178	2	Q82KL4	Q82kl4 streptomyce	332	23	100.0	197	2	Q7QB52	Q7qb52 anopheles g
260	23	100.0	180	1	I17B HUMAN	Q8uhf5 homo sapien	333	23	100.0	198	2	O8SS16	Q8ss16 encephalito
261	23	100.0	180	2	Q6IAG3	Q6ia93 homo sapien	334	23	100.0	198	2	Q9P0P4	Q9p0p4 homo sapien
262	23	100.0	180	2	Q82GM2	Q82gm2 streptomyce	335	23	100.0	198	2	Q8HYS2	Q8hye2 sus scrofa
263	23	100.0	181	2	Q7KW93	Q7kw93 drosophila	336	23	100.0	198	2	O84371	Q84371 insertion s
264	23	100.0	182	2	Q6C678	Q6c678 yarrowia li	337	23	100.0	198	2	Q8R614	Q8r614 agrobacteri
265	23	100.0	182	2	Q9TNR3	Q9tnr3 macaca mula	338	23	100.0	198	2	O8NQN8	O8nqn8 corynebacte
266	23	100.0	182	2	Q89IJ8	Q89ij8 bradyrhizob	339	23	100.0	198	2	Q98J07	Q98j07 rhizobium l
267	23	100.0	182	2	Q9DXK3	Q9dk83 human immun	340	23	100.0	198	2	Q9JUF5	Q9juf5 mus musculus
268	23	100.0	183	2	Q6FSI2	Q6fsi2 candida gla	341	23	100.0	199	2	O6A9G7	Q6a9g7 propionbac
269	23	100.0	183	2	Q7SFK1	Q7sfk1 neurospora	342	23	100.0	200	2	Q9C2F1	Q9c2f1 neurospora
270	23	100.0	183	2	Q7SFK1	Q7sfk1 neurospora	343	23	100.0	200	2	O6IPX3	Q6ipx3 homo sapien
271	23	100.0	184	2	O8VY57	O8vy57 arabidopsis	344	23	100.0	200	2	Q97N20	Q97n20 clostridium
272	23	100.0	184	2	Q93V31	Q93v31 arabidopsis	345	23	100.0	201	2	Q7QJ59	Q7qj59 anopheles g
273	23	100.0	184	2	O6K425	O6k425 oryza sativ	346	23	100.0	201	2	Q93QF9	Q93qf9 brevbacter
274	23	100.0	184	2	Q7XWY1	Q7xwy1 oryza sativ	347	23	100.0	201	2	Q9R6L7	Q9r6l7 agrobacteri
275	23	100.0	184	2	Q9A997	Q9a997 caulobacter	348	23	100.0	201	2	Q97JF7	Q97jf7 clostridium
276	23	100.0	184	2	Q6D0Z8	Q6d0z8 erwinia car	349	23	100.0	201	2	Q9I6B8	Q9i6b8 pseudomonas
277	23	100.0	184	2	Q9D6D4	Q9d6d4 mus musculus	350	23	100.0	201	2	O6S865	O6s865 barley yell
278	23	100.0	185	2	O18237	O18237 caenorhabdi	351	23	100.0	201	2	O8JIX9	O8jix9 gallus gall
279	23	100.0	185	2	Q96S81	Q96s81 caenorhabdi	352	23	100.0	201	2	O8JUY0	O8jiy0 gallus gall
280	23	100.0	185	2	O86F33	Q86f33 schistosoma	353	23	100.0	201	2	Q76EY7	Q76ey7 gallus gall
281	23	100.0	185	2	O69909	Q69909 streptomyce	354	23	100.0	202	2	Q92R27	Q92r27 rhizobium m
282	23	100.0	185	2	Q725T8	Q725t8 desulfovibr	355	23	100.0	202	2	Q7VY11	Q7vy11 bordetella
283	23	100.0	185	2	O82TC6	O82tc6 nitrosomona	356	23	100.0	202	2	Q7W749	Q7w749 bordetella
284	23	100.0	186	2	Q96BM9	Q96bm9 homo sapien	357	23	100.0	202	2	Q7WIN3	Q7win3 bordetella
285	23	100.0	186	2	Q9NVJ2	Q9nvj2 homo sapien	358	23	100.0	203	2	Q4LH6	Q4lh6 oryza sativ
286	23	100.0	186	2	Q7PQM1	Q7pqm1 anopheles g	359	23	100.0	203	2	O84R02	Q84r02 oryza sativ
287	23	100.0	186	2	Q9VHV5	Q9vhv5 drosophila	360	23	100.0	203	2	Q9QIX6	Q9qix6 olive leaf
288	23	100.0	186	2	O8RPT7	O8rpt7 uncultured	361	23	100.0	204	2	O8NAZ9	O8naz9 homo sapien
289	23	100.0	186	2	O877T9	O87t9 xylella fas	362	23	100.0	204	2	O6LSD0	O6lsd0 photobacter
290	23	100.0	186	2	Q9PCS3	Q9pcs3 xylella fas	363	23	100.0	204	2	Q7U578	Q7u578 synechococc
291	23	100.0	186	2	Q66HA6	Q66ha6 rattus norv	364	23	100.0	204	2	Q9WZD7	Q9wz7 thermotoga
292	23	100.0	186	2	Q8VEH3	Q8veh3 mus musculus	365	23	100.0	204	2	Q7TS73	Q7ts73 mus musculus
293	23	100.0	186	2	Q9CQM2	Q9cqmw2 m mus muscu	366	23	100.0	205	2	O87BM2	Q87bm2 xylella fas
294	23	100.0	186	2	Q6NZW8	Q6nzw8 brachydanio	367	23	100.0	205	2	Q9PAT9	Q9pat9 xylella fas
295	23	100.0	186	2	O6NZ23	Q6nzz3 brachydanio	368	23	100.0	205	2	O9PAU3	Q9pau3 xylella fas
296	23	100.0	186	2	O6P8C8	Q6p8c8 xenopus tro	369	23	100.0	205	2	O8QP41	Q8qp41 potato leaf
297	23	100.0	187	2	Q9BVQ2	Q9bvq2 homo sapien	370	23	100.0	206	1	ATKC XANAC	Q8ppc8 xanthomonas
298	23	100.0	187	2	Q7XSA1	Q7xsa1 oryza sativ	371	23	100.0	206	2	Q96FE3	Q96fe3 homo sapien
299	23	100.0	188	2	O68834	Q68834 francisella	372	23	100.0	207	1	YQJI ECOLI	Yqji ecoli
300	23	100.0	188	2	Q9AGY1	Q9agy1 lactococcus	373	23	100.0	207	1	YQJI_SHIFL	Yqji shifl
301	23	100.0	188	2	Q7NPM7	Q7npw7 chromobacte	374	23	100.0	207	2	O8MTM3	Q8mtm3 branchiosto
302	23	100.0	188	2	O6PBM8	Q6pbm8 brachydanio	375	23	100.0	207	2	Q7DM40	Q7dm40 pinus sylve
303	23	100.0	189	2	Q7WZ71	Q7wz71 bordetella	376	23	100.0	207	2	Q9LY40	Q9ly40 arabidopsis
304	23	100.0	189	2	Q7WR37	Q7wr37 bordetella	377	23	100.0	207	2	O8FDF9	O8fdf9 escherichia
305	23	100.0	189	2	O6AC03	Q6ac03 leifsonia x	378	23	100.0	207	2	O8XAN2	O8xan2 escherichia
306	23	100.0	190	2	Q96H35	Q96h35 homo sapien	379	23	100.0	207	2	Q9DM27	Q9dm27 rat cytomeg
307	23	100.0	190	2	Q6ZP92	Q6zpz2 homo sapien	380	23	100.0	208	1	COAT_PLRV	Coat plrv
308	23	100.0	190	2	Q75IA8	Q75ia8 oryza sativ	381	23	100.0	208	1	COAT_PLRV1	Coat plrv1
309	23	100.0	190	2	Q9M2X1	Q9m2x1 arabidopsis	382	23	100.0	208	1	COAT_PLRV1	Coat plrv1
310	23	100.0	190	2	Q8CBDA	Q8cbda mus musculus	383	23	100.0	208	1	COAT_PLRVW	Coat plrvw
311	23	100.0	190	2	Q9CR83	Q9cr83 m mus muscu	384	23	100.0	208	2	O8N282	O8n282 homo sapien
312	23	100.0	190	2	O66J99	Q66j99 xenopus lae	385	23	100.0	208	2	Q9VJF3	Q9vjf3 drosophila
313	23	100.0	191	1	CLP1 CHLCV	Q824c7 chlamydomophi	386	23	100.0	208	2	O6F3C6	O6f3c6 oryza sativ
314	23	100.0	191	2	Q9BZV4	Q9bzv4 homo sapien	387	23	100.0	208	2	Q49140	Q49140 methylobact
315	23	100.0	191	2	Q940L1	Q940l1 arabidopsis	388	23	100.0	208	2	O9RV47	O9rv47 deinococcus
316	23	100.0	191	2	Q7XMK2	Q7xmk2 oryza sativ	389	23	100.0	208	2	O37936	O37936 potato leaf
317	23	100.0	191	2	Q9RX62	Q9rx62 deinococcus	390	23	100.0	208	2	O8QYN7	O8qyn7 potato leaf
318	23	100.0	191	2	Q90VK2	Q90vk2 human immun	391	23	100.0	208	2	O8QYN7	O8qyn7 potato leaf
319	23	100.0	192	2	O6YWB7	Q6ywb7 oryza sativ	392	23	100.0	208	2	O8QYQ0	O8qyq0 potato leaf
320	23	100.0	192	2	Q7P0F9	Q7p0f9 chromobacte	393	23	100.0	208	2	O8QYR9	O8qyr9 potato leaf
321	23	100.0	193	2	O6G4K6	Q6g4k6 bartonella	394	23	100.0	208	2	O99GS3	O99gs3 potato leaf
322	23	100.0	194	2	Q7SC18	Q7sc18 neurospora	395	23	100.0	208	2	O99GS6	O99gs6 potato leaf
323	23	100.0	195	2	Q52719	Q52719 rhodobacter	396	23	100.0	208	2	Q76QV9	Q76qv9 potato leaf

397	23	100.0	208	2	Q84814	Q84814 potato leaf	470	23	100.0	220	2	Q7QKS4	Q7QKS4 anopheles g
398	23	100.0	208	2	Q84821	Q84821 potato leaf	471	23	100.0	220	2	Q8VLR2	Q8VLR2 bordetella
399	23	100.0	208	2	Q84823	Q84823 potato leaf	472	23	100.0	220	2	Q989P7	Q989P7 rhizobium l
400	23	100.0	208	2	Q84827	Q84827 potato leaf	473	23	100.0	220	2	Q82BH6	Q82BH6 streptomyce
401	23	100.0	208	2	Q84838	Q84838 potato leaf	474	23	100.0	221	2	Q36717	Q36717 synechococ
402	23	100.0	208	2	Q86898	Q86898 potato leaf	475	23	100.0	221	2	Q9R6T5	Q9R6T5 synechococ
403	23	100.0	208	2	Q8BC79	Q8BC79 potato leaf	476	23	100.0	221	2	Q8YXH1	Q8YXH1 anabaena sp
404	23	100.0	208	2	Q9DKJ1	Q9DKJ1 potato leaf	477	23	100.0	221	2	Q7NEY5	Q7NEY5 gloeobacter
405	23	100.0	208	2	Q9YNY4	Q9YNY4 potato leaf	478	23	100.0	221	2	Q8VAT8	Q8VAT8 monkeypox v
406	23	100.0	209	1	ATKC_XANCP	Q8PCMO xanthomonas	479	23	100.0	222	2	Q6CG04	Q6CG04 yarrowia li
407	23	100.0	209	2	Q8LDR7	Q8LDR7 arabidopsis	480	23	100.0	222	2	Q67NE7	Q67NE7 symbiobacte
408	23	100.0	209	2	Q8W115	Q8W115 arabidopsis	481	23	100.0	222	2	Q8PD41	Q8PD41 xanthomonas
409	23	100.0	209	2	Q9LZW7	Q9LZW7 arabidopsis	482	23	100.0	222	2	Q8AVA2	Q8AVA2 brachydanio
410	23	100.0	210	2	Q94113	Q94113 oryza sativ	483	23	100.0	223	2	Q8IR09	Q8IR09 drosophila
411	23	100.0	210	2	Q7XG29	Q7XG29 oryza sativ	484	23	100.0	223	2	Q61LY3	Q61LY3 drosophila
412	23	100.0	210	2	Q98226	Q98226 rhizobium l	485	23	100.0	223	2	Q9NHC0	Q9NHC0 drosophila
413	23	100.0	210	2	Q7V8A8	Q7V8A8 prochloroco	486	23	100.0	223	2	Q668I8	Q668I8 bacteroides
414	23	100.0	211	2	Q8YOV0	Q8YOV0 ralstonia s	487	23	100.0	223	2	Q64TH2	Q64TH2 yersinia ps
415	23	100.0	212	1	YQ15_CAEEL	Q92330 caenorhabdi	488	23	100.0	223	2	Q8JL79	Q8JL79 ectromelia
416	23	100.0	212	2	Q94997	Q94997 homo sapien	489	23	100.0	224	1	GPX3_CAEEL	Q95003 caenorhabdi
417	23	100.0	212	2	Q71MF6	Q71MF6 homo sapien	490	23	100.0	224	2	Q7PE62	Q7PE62 anopheles g
418	23	100.0	212	2	Q9NTK1	Q9NTK1 homo sapien	491	23	100.0	224	2	Q9B0G1	Q9B0G1 staphylococ
419	23	100.0	212	2	Q7JMK4	Q7JMK4 caenorhabdi	492	23	100.0	224	2	Q9LH67	Q9LH67 arabidopsis
420	23	100.0	212	2	Q67WM8	Q67WM8 oryza sativ	493	23	100.0	224	2	Q54545	Q54545 escherichia
421	23	100.0	212	2	Q8PQ13	Q8PQ13 xanthomonas	494	23	100.0	224	2	Q823V9	Q823V9 salmonella
422	23	100.0	212	2	Q8C5F6	Q8C5F6 mus musculu	495	23	100.0	224	2	Q90PW7	Q90PW7 chimpanzee
423	23	100.0	213	2	Q9HFP4	Q9HFP4 schizophyll	496	23	100.0	225	2	Q8XCA3	Q8XCA3 escherichia
424	23	100.0	213	2	Q76MX8	Q76MX8 homo sapien	497	23	100.0	225	2	Q6N4G7	Q6N4G7 rhodopseudo
425	23	100.0	213	2	Q9NSM1	Q9NSM1 homo sapien	498	23	100.0	225	2	Q825R9	Q825R9 streptomyce
426	23	100.0	213	2	Q6WAZ5	Q6WAZ5 trypanosoma	499	23	100.0	226	2	Q724Y3	Q724Y3 homo sapien
427	23	100.0	213	2	Q7XTL6	Q7XTL6 oryza sativ	500	23	100.0	226	2	Q54683	Q54683 lactococcus
428	23	100.0	213	2	Q7D766	Q7D766 mycobacteri	501	23	100.0	226	2	P96049	P96049 streptococ
429	23	100.0	213	2	Q53480	Q53480 mycobacteri	502	23	100.0	226	2	Q48649	Q48649 lactococcus
430	23	100.0	213	2	Q7TZ38	Q7TZ38 mycobacteri	503	23	100.0	226	2	Q48653	Q48653 lactococcus
431	23	100.0	213	2	Q7U8Q3	Q7U8Q3 synechococ	504	23	100.0	226	2	Q48716	Q48716 lactococcus
432	23	100.0	213	2	Q9RW35	Q9RW35 deinococcus	505	23	100.0	226	2	Q52090	Q52090 lactococcus
433	23	100.0	213	2	Q6XD14	Q6XD14 sciurus car	506	23	100.0	226	2	Q54350	Q54350 lactococcus
434	23	100.0	214	2	Q623V7	Q623V7 oryza sativ	507	23	100.0	226	2	Q54352	Q54352 lactococcus
435	23	100.0	214	2	Q8PHB3	Q8PHB3 xanthomonas	508	23	100.0	226	2	Q7BLH4	Q7BLH4 lactococcus
436	23	100.0	215	2	Q9N630	Q9N630 drosophila	509	23	100.0	226	2	Q7BLP1	Q7BLP1 lactococcus
437	23	100.0	215	2	Q8P5Z5	Q8P5Z5 xanthomonas	510	23	100.0	226	2	Q9L649	Q9L649 lactococcus
438	23	100.0	215	2	Q99JQ3	Q99JQ3 mus musculu	511	23	100.0	226	2	Q9R491	Q9R491 lactococcus
439	23	100.0	216	2	Q9YCU3	Q9YCU3 aeropyrum p	512	23	100.0	226	2	Q9R7J1	Q9R7J1 lactococcus
440	23	100.0	216	2	Q6BM58	Q6BM58 debaryomyce	513	23	100.0	226	2	Q742R4	Q742R4 mycobacteri
441	23	100.0	216	2	Q6FLG6	Q6FLG6 candida gla	514	23	100.0	227	1	EMBP_RAT	Q63189 ratus norv
442	23	100.0	216	2	Q8NSC9	Q8NSC9 homo sapien	515	23	100.0	227	2	Q9HMV3	Q9HMV3 halobacteri
443	23	100.0	216	2	Q6N1A9	Q6N1A9 rhodopseudo	516	23	100.0	227	2	Q6L025	Q6L025 picrophilus
444	23	100.0	217	2	Q754Y4	Q754Y4 ashbya goss	517	23	100.0	227	2	Q7F2F0	Q7F2F0 oryza sativ
445	23	100.0	217	2	Q85613	Q85613 escherichia	518	23	100.0	227	2	Q9ZFX1	Q9ZFX1 pseudomonas
446	23	100.0	217	2	Q7A9R9	Q7A9R9 escherichia	519	23	100.0	227	2	Q63W09	Q63W09 burkholderi
447	23	100.0	217	2	Q6AAB7	Q6AAB7 propionibac	520	23	100.0	228	1	NANE_LACPL	P59441 lactobacill
448	23	100.0	217	2	Q80FI4	Q80FI4 goose hemor	521	23	100.0	228	1	RP1A_RALSO	Q8Y013 ralstonia s
449	23	100.0	218	1	VA41_VARV	P33854 variola vir	522	23	100.0	228	2	Q63613	Q63613 balanogloss
450	23	100.0	218	2	Q8QMR3	Q8QMR3 cowpox viru	523	23	100.0	229	2	Q979E2	Q979E2 thermoplasm
451	23	100.0	218	2	Q85397	Q85397 variola maj	524	23	100.0	229	2	Q92X28	Q92X28 mycobacteri
452	23	100.0	218	2	Q9QNH4	Q9QNH4 variola min	525	23	100.0	229	2	Q6M463	Q6M463 corynebacte
453	23	100.0	218	2	Q903H6	Q903H6 human immun	526	23	100.0	229	2	Q8XMU6	Q8XMU6 enterococcu
454	23	100.0	219	1	UPPS_AERPE	Q9YC66 aeropyrum p	527	23	100.0	229	2	Q9D6E8	Q9D6E8 mus musculu
455	23	100.0	219	1	VA41_VACCC	P21064 vaccinia vi	528	23	100.0	230	2	Q8U0G0	Q8U0G0 pyrococcus
456	23	100.0	219	1	VA41_VACCV	P24766 vaccinia vi	529	23	100.0	230	2	Q92290	Q92290 rhizobium m
457	23	100.0	219	2	Q8NYG0	Q8NYG0 staphylococ	530	23	100.0	230	2	Q87DV2	Q87DV2 xylella fas
458	23	100.0	219	2	Q99WU9	Q99WU9 staphylococ	531	23	100.0	230	2	Q9RXX7	Q9RXX7 streptomyce
459	23	100.0	219	2	Q7A7S9	Q7A7S9 staphylococ	532	23	100.0	231	2	Q9HJH9	Q9HJH9 thermoplasm
460	23	100.0	219	2	Q6GCU5	Q6GCU5 staphylococ	533	23	100.0	231	2	Q873D3	Q873D3 neurospora
461	23	100.0	219	2	Q6GK34	Q6GK34 staphylococ	534	23	100.0	231	2	Q9MBS0	Q9MBS0 staphylococ
462	23	100.0	219	2	Q57242	Q57242 vaccinia vi	535	23	100.0	231	2	Q8W4A6	Q8W4A6 arabidopsis
463	23	100.0	219	2	Q8V2L7	Q8V2L7 camelpox vi	536	23	100.0	231	2	Q7D7K8	Q7D7K8 mycobacteri
464	23	100.0	219	2	Q6RZE2	Q6RZE2 rabbitpox v	537	23	100.0	232	1	DEF_DEIRA	Q9RRQ4 deinococcus
465	23	100.0	219	2	Q76ZN6	Q76ZN6 vaccinia vi	538	23	100.0	232	1	VSRT_BOTJA	P81824 bothrops ja
466	23	100.0	219	2	Q775N8	Q775N8 camelpox vi	539	23	100.0	232	2	Q81X71	Q81X71 methanopyru
467	23	100.0	219	2	Q77TH2	Q77TH2 vaccinia vi	540	23	100.0	232	2	Q87228	Q87228 lactococcus
468	23	100.0	219	2	Q80DT5	Q80DT5 cowpox viru	541	23	100.0	232	2	Q741F6	Q741F6 mycobacteri
469	23	100.0	219	2	Q9IVC3	Q9IVC3 human immun	542	23	100.0	232	2	Q82TK3	Q82TK3 nitrosomona

543	23	100.0	233	2	O59233	O59233 pyrococcus	616	23	100.0	250	2	Q87064	Q87064 suid herpes
544	23	100.0	233	2	Q8PYV0	Q8PYV0 methanosarc	617	23	100.0	250	2	Q64EY8	Q64EY8 pea enation
545	23	100.0	233	2	Q8TIF0	Q8TIF0 methanosarc	618	23	100.0	251	1	UPPS_VIBVU	Q8dbf7 vibrio vuln
546	23	100.0	233	2	O9V178	O9V178 pyrococcus	619	23	100.0	251	1	UPPS_VIBVY	Q7m1q4 vibrio vuln
547	23	100.0	233	2	O8NP51	O8NP51 corynebacte	620	23	100.0	251	1	Q72C96	Q72c96 desulfovibr
548	23	100.0	234	2	O6BYW0	O6BYW0 debaryomyce	621	23	100.0	252	1	NXP3_HUMAN	O95157 homo sapien
549	23	100.0	234	2	Q9SDS2	Q9SDS2 rhizobium m	622	23	100.0	252	1	NXP3_MOUSE	Q91vx5 mus musculu
550	23	100.0	235	2	O9SRS2	O9SRS2 rhizobium m	623	23	100.0	252	1	NXP3_RAT	Q92n5 rattus norv
551	23	100.0	235	2	O9JMW6	O9JMW6 arabidopsis	624	23	100.0	252	2	Q6ZQR4	Q6zqr4 homo sapien
552	23	100.0	235	2	O8ZM66	O8ZM66 bradyrhizob	625	23	100.0	252	2	Q84VC6	Q84vc6 oryza sativ
553	23	100.0	235	2	O9CU42	O9CU42 salmoneilla	626	23	100.0	252	2	Q92MS9	Q92ms9 rhizobium m
554	23	100.0	236	2	O54351	O54351 mus musculu	627	23	100.0	252	2	Q7UK23	Q7uk23 rhodopirell
555	23	100.0	237	2	O94351	O94351 lactococcus	628	23	100.0	252	2	Q7UK24	Q7uk24 rhodopirell
556	23	100.0	237	2	O9HN39	O9HN39 halobacteri	629	23	100.0	253	2	Q7U5H3	Q7u5h3 synechococc
557	23	100.0	238	2	O9FWM5	O9FWM5 arabidopsis	630	23	100.0	253	2	Q9RRZ8	Q9rrz8 deinococcus
558	23	100.0	238	2	Q96BP7	Q96BP7 homo sapien	631	23	100.0	253	2	Q9D1D1	Q9d1d1 m mus muscu
559	23	100.0	238	2	Q96D31	Q96D31 homo sapien	632	23	100.0	254	1	S5A2_PIG	O18765 sus scrofa
560	23	100.0	238	2	Q8H0L2	Q8H0L2 triticum ae	633	23	100.0	254	2	Q8T4Q4	Q8t4q4 aedes aegyp
561	23	100.0	238	2	Q8U7D4	Q8U7D4 agrobacteri	634	23	100.0	254	2	Q8T4Q5	Q8t4q5 aedes aegyp
562	23	100.0	238	2	Q7VWB7	Q7VWB7 bordetella	635	23	100.0	254	2	Q95PA3	Q95pa3 aedes aegyp
563	23	100.0	238	2	Q7W9G9	Q7W9G9 bordetella	636	23	100.0	254	2	Q95PA6	Q95pa6 aedes aegyp
564	23	100.0	238	2	Q7WGZ9	Q7WGZ9 bordetella	637	23	100.0	254	2	O94GQ5	Q94gq5 oryza sativ
565	23	100.0	238	2	Q87VM1	Q87VM1 pseudomonas	638	23	100.0	254	2	Q7WC99	Q7wc99 bordetella
566	23	100.0	238	2	Q88DG2	Q88DG2 pseudomonas	639	23	100.0	254	2	Q820W4	Q820w4 coxiella bu
567	23	100.0	238	2	Q9HUQ4	Q9HUQ4 pseudomonas	640	23	100.0	255	2	Q7CV55	Q7cv55 agrobacteri
568	23	100.0	239	1	6PGL_SYNY3	P74618 synechocyst	641	23	100.0	255	2	Q6LH36	Q6lh36 photobacter
569	23	100.0	239	2	Q69WM3	Q69wm3 oryza sativ	642	23	100.0	255	2	Q7NR85	Q7nr85 chromobacte
570	23	100.0	239	2	Q8C9T0	Q8C9T0 mus musculu	643	23	100.0	255	2	Q9RZP2	Q9rzp2 deinococcus
571	23	100.0	240	2	Q8SOH2	Q8SOH2 oryza sativ	644	23	100.0	255	2	Q9VC12	Q9vc12 mus musculu
572	23	100.0	240	2	Q8VK02	Q8VK02 mycobacteri	645	23	100.0	256	1	ATPF_MOUSE	Q8vcq7 mus musculu
573	23	100.0	240	2	Q72HH7	Q72hh7 thermus the	646	23	100.0	256	1	ATPF_RAT	P19511 rattus norv
574	23	100.0	241	2	Q8H4H6	Q8H4h6 oryza sativ	647	23	100.0	256	2	Q92VY2	Q92vy2 rhizobium m
575	23	100.0	241	2	Q9ZSU0	Q9Zsu0 oryza sativ	648	23	100.0	256	2	Q90LS3	Q90ls3 human immun
576	23	100.0	241	2	Q6ZZN6	Q6zzn6 streptomyce	649	23	100.0	257	2	Q7NR11	Q7nr11 chromobacte
577	23	100.0	241	2	Q8DUJ24	Q8dj24 synechococc	650	23	100.0	258	1	VSP2_TRIJE	Q8df67 trimeresuru
578	23	100.0	241	2	Q6ARJ4	Q6ap74 desulfotale	651	23	100.0	258	2	Q96K19	Q96k19 homo sapien
579	23	100.0	242	2	Q8DH96	Q8dh96 synechococc	652	23	100.0	258	2	Q92XH6	Q92xh6 rhizobium m
580	23	100.0	242	2	Q9DSA5	Q9dsa5 mus musculu	653	23	100.0	258	2	Q7U4F8	Q7u4f8 synechococc
581	23	100.0	243	1	RS3_SYNP6	Q24695 synechococc	654	23	100.0	258	2	Q90ZN2	Q90zn2 gallus gall
582	23	100.0	243	1	Y91E_METJA	O58322 methanococc	655	23	100.0	259	2	Q6L203	Q6l203 picrophilus
583	23	100.0	243	1	ZIPA_XANAC	Q6pmi0 xanthomonas	656	23	100.0	259	2	Q8BWS5	Q8bw5 vibrio vuln
584	23	100.0	243	1	Q6S8A8	Q6s8a8 comamonas s	657	23	100.0	260	1	VSP2_TRIFL	Q13057 trimeresuru
585	23	100.0	243	2	Q7W6U7	Q7w6u7 bordetella	658	23	100.0	260	1	VSPA_TRIGA	O13060 trimeresuru
586	23	100.0	243	2	Q7WHT5	Q7wht5 bordetella	659	23	100.0	260	2	Q9UG54	Q9ug54 homo sapien
587	23	100.0	243	2	Q9PFD1	O9pfd1 xylella fas	660	23	100.0	260	2	Q8XQ22	Q8xq22 ralstonia s
588	23	100.0	244	2	Q61763	O61763 caenorhabdi	661	23	100.0	260	2	Q88F08	Q88fu8 pseudomonas
589	23	100.0	244	2	Q8Z1U5	Q8z1u5 salmonella	662	23	100.0	260	2	Q9HXM0	Q9hxm0 pseudomonas
590	23	100.0	245	1	CIQA_MOUSE	P98086 mus musculu	663	23	100.0	260	2	Q71QI0	Q71qi0 trimeresuru
591	23	100.0	245	1	XJBG_ECOLI	P32688 escherichia	664	23	100.0	261	2	O24230	O24230 oryza sativ
592	23	100.0	245	2	Q7QD70	Q7qdi0 anopheles g	665	23	100.0	261	2	Q9AV20	Q9av20 oryza sativ
593	23	100.0	245	2	Q40512	Q40512 nicotiana t	666	23	100.0	261	2	Q8LIU3	Q8liu3 bordetella
594	23	100.0	245	2	Q9SDM1	Q9sdm1 hordeum vul	667	23	100.0	261	2	P74291	P74291 synechocyst
595	23	100.0	245	2	Q8ZK12	Q8zk12 salmonella	668	23	100.0	261	2	Q6VY34	Q6vy34 turkey astr
596	23	100.0	245	2	Q741I0	Q741i0 mycobacteri	669	23	100.0	262	2	O8L3X8	O8l3x8 arabidopsis
597	23	100.0	245	2	Q89K04	Q89k04 bradyrhizob	670	23	100.0	262	2	Q9FYA9	Q9fya9 arabidopsis
598	23	100.0	245	2	Q8CVI7	O8cvi7 escherichia	671	23	100.0	262	2	Q87818	Q87818 roseobacte
599	23	100.0	245	2	Q83IP2	Q83ip2 shigella fl	672	23	100.0	262	2	Q98LJ1	Q98lj1 rhizobium l
600	23	100.0	245	2	Q8X5X9	Q8x5x9 escherichia	673	23	100.0	262	2	Q88D49	Q88d49 pseudomonas
601	23	100.0	245	2	Q9DCM6	Q9dcm6 m mus muscu	674	23	100.0	263	1	SSB_THETH	O85824 thermus the
602	23	100.0	246	1	CB11_LYCES	P12360 lycopersico	675	23	100.0	263	2	Q619R6	Q619r6 homo sapien
603	23	100.0	246	2	O20269	Q20269 pinus sylve	676	23	100.0	263	2	Q70M05	Q70m05 thermus the
604	23	100.0	246	2	Q9FY07	Q9fy07 pisum sativ	677	23	100.0	263	2	Q8XRG2	Q8xrg2 ralstonia s
605	23	100.0	246	2	Q6N9V7	Q6n9v7 rhodopseudo	678	23	100.0	263	2	Q92VA5	Q92va5 rhizobium m
606	23	100.0	246	2	Q89IP6	Q89ip6 bradyrhizob	679	23	100.0	263	2	Q72GV7	Q72gv7 thermus the
607	23	100.0	247	2	Q86486	O98486 streptomyce	680	23	100.0	263	2	Q7UUN7	Q7ujn7 rhodopirell
608	23	100.0	247	2	Q988V3	Q988v3 rhizobium l	681	23	100.0	263	2	Q82BQ9	Q82bg9 streptomyce
609	23	100.0	247	2	Q7NSP7	Q7nsp7 chromobacte	682	23	100.0	264	1	LE34_GOSHI	P09444 gossypium h
610	23	100.0	248	2	Q92ZB2	Q92zb2 rhizobium m	683	23	100.0	264	1	SSB_THETAQ	Q9kh06 thermus aqu
611	23	100.0	248	2	Q73TX5	Q73tx5 mycobacteri	684	23	100.0	264	2	Q8IT87	Q8iy87 homo sapien
612	23	100.0	249	2	Q82V15	Q82v15 nitrosomona	685	23	100.0	264	2	Q63MM9	Q63mm9 burkholderi
613	23	100.0	249	2	Q810I0	Q810i0 mus musculu	686	23	100.0	265	2	O61218	O61218 caenorhabdi
614	23	100.0	250	2	Q8BPF7	Q8bpf7 uncultured	687	23	100.0	265	2	Q9RHH3	Q9rhh3 porphyromon
615	23	100.0	250	2	Q84696	Q84696 pea enation	688	23	100.0	265	2	Q64RU7	Q64ru7 bacteroides

689	23	100.0	265	2	Q8PQ61	O8pq61 xanthomonas	762	23	100.0	283	2	Q7CRQ0	Q7crq0 agrobacteri
690	23	100.0	265	2	Q8UB74	O8ub74 agrobacteri	763	23	100.0	283	2	Q8G9K1	Q8g9k1 uncultured
691	23	100.0	285	2	Q6LUJ7	Q6luj7 photobacter	764	23	100.0	283	2	Q8APR3	Q8apx3 ralstonia s
692	23	100.0	285	2	Q72FZ8	Q72fz8 desulfovibr	765	23	100.0	283	2	Q97CW7	Q97cw7 clostridium
693	23	100.0	266	2	Q9HG11	O9hg11 homo sapien	766	23	100.0	284	2	Q8NFB6	Q8nfb6 homo sapien
694	23	100.0	266	2	Q9XGW2	O9xgw2 rosa hybrid	767	23	100.0	284	2	Q6F2D3	Q6f2d3 solanum dem
695	23	100.0	266	2	Q4G059	Q4g059 corynebacte	768	23	100.0	285	2	Q60501	Q60501 cricetus
696	23	100.0	266	2	Q91AV8	Q91av8 pseudomonas	769	23	100.0	286	2	Q872G3	Q872g3 neurospora
697	23	100.0	266	2	Q7SZN2	Q7szn2 brachydanio	770	23	100.0	286	2	Q712J0	Q712j0 rattus norv
698	23	100.0	267	2	Q6FF63	Q6ff63 acinetobact	771	23	100.0	286	2	Q8CBG9	Q8cbg9 mus musculu
699	23	100.0	268	2	Q6NXA8	Q6nxa8 brachydanio	772	23	100.0	287	2	Q9XTT1	Q9xtt1 caenorhabdi
700	23	100.0	269	1	Y374 MYCPN	Y75226 mycoplasma	773	23	100.0	287	2	Q69X10	Q69x10 cryza sativ
701	23	100.0	269	2	Q7PTI5	Q7pti5 anopheles g	774	23	100.0	287	2	Q9ZAY6	Q9zay6 anabaena sp
702	23	100.0	269	2	Q7R778	Q7r778 plasmodium	775	23	100.0	287	2	Q8VKR7	Q8vkr7 mycobacteri
703	23	100.0	269	2	Q8YU16	Q8yul6 anabaena sp	776	23	100.0	287	2	Q72EU0	Q72eu0 desulfovibr
704	23	100.0	269	2	Q7W070	Q7w070 bordetella	777	23	100.0	287	2	Q72UT8	Q72ut8 brachydanio
705	23	100.0	269	2	Q7WQA3	Q7wqa3 bordetella	778	23	100.0	288	2	O52588	O52588 mycobacteri
706	23	100.0	270	2	Q6RHA6	Q6rha6 paracoccus	779	23	100.0	289	1	Q717 HUMAN	Q717 human
707	23	100.0	271	2	Q86LV6	Q86lv6 brachioslo	780	23	100.0	289	2	Q924Z2	Q924z2 streptomyc
708	23	100.0	271	2	Q80611	Q80611 arabidopsis	781	23	100.0	289	2	Q8BVD7	Q8bvd7 mus musculu
709	23	100.0	271	2	Q942X1	Q942x1 cryza sativ	782	23	100.0	290	1	GC3 HUMAN	P01860 homo sapien
710	23	100.0	271	2	Q6QF95	Q6qf95 triticum ae	783	23	100.0	290	2	Q6ZAN8	Q6zan8 cryza sativ
711	23	100.0	271	2	Q9ZRR4	Q9zrr4 triticum ae	784	23	100.0	290	2	Q79T09	Q79t09 pseudomonas
712	23	100.0	271	2	Q8GJK5	Q8gjk5 synchococc	785	23	100.0	290	2	Q910X2	Q910x2 pseudomonas
713	23	100.0	271	2	Q828S9	Q828s9 streptomyc	786	23	100.0	290	2	Q75B33	Q75b33 ashbya goss
714	23	100.0	272	1	PROC PSEAE	P22008 pseudomonas	787	23	100.0	291	2	Q72LR5	Q72lr5 leptospira
715	23	100.0	272	2	Q933D8	Q933d8 haemophilus	788	23	100.0	291	2	Q89M83	Q89m83 bradyrhizob
716	23	100.0	272	2	Q93T06	Q93t06 haemophilus	789	23	100.0	291	2	Q8EY71	Q8ey71 leptospira
717	23	100.0	272	2	Q93T08	Q93t08 haemophilus	790	23	100.0	292	2	Q7QOH8	Q7qoh8 giardia lam
718	23	100.0	272	2	Q93T10	Q93t10 haemophilus	791	23	100.0	292	2	Q9VRB7	Q9vrb7 drosophila
719	23	100.0	272	2	Q8UA67	Q8ua67 agrobacteri	792	23	100.0	292	2	Q6H077	Q6h077 fremyella d
720	23	100.0	272	2	Q8VYX0	Q8vyx0 anabaena sp	793	23	100.0	292	2	Q88IN8	Q88in8 pseudomonas
721	23	100.0	272	2	Q8BJ72	Q8bj72 mus musculu	794	23	100.0	292	2	Q89QZ3	Q89qz3 bradyrhizob
722	23	100.0	273	2	Q6QF97	Q6qf97 triticum ae	795	23	100.0	292	2	Q8HZC6	Q8hzc6 macaca sp.
723	23	100.0	273	2	Q93T07	Q93t07 haemophilus	796	23	100.0	293	2	Q8HU10	Q8hu10 pseudomonas
724	23	100.0	273	2	Q93T09	Q93t09 haemophilus	797	23	100.0	293	2	Q8N4U8	Q8n4u8 homo sapien
725	23	100.0	274	1	RK2 OENHO	O9mdu0 oenothera h	798	23	100.0	294	2	Q86WE8	Q86we8 homo sapien
726	23	100.0	274	2	Q7Q305	Q7q305 anopheles g	799	23	100.0	294	2	Q6X3K8	Q6x3k8 pseudomonas
727	23	100.0	274	2	Q8QNB8	Q8qnb8 ectocarpus	800	23	100.0	294	2	Q8CFT0	Q8cft0 mus musculu
728	23	100.0	275	1	DHPS_HAEIN	F43776 haemophilus	801	23	100.0	294	2	Q9P744	Q9p744 neurospora
729	23	100.0	275	2	Q65TY7	Q65ty7 manheimia	802	23	100.0	295	2	Q7F262	Q7f262 cryza sativ
730	23	100.0	276	2	Q6PJP7	Q6pjp7 homo sapien	803	23	100.0	296	2	Q7F262	Q7f262 cryza sativ
731	23	100.0	276	2	Q7MI03	Q7mi03 vibrio vuln	804	23	100.0	297	2	P17437	P17437 caenorhabdi
732	23	100.0	276	2	Q82EM4	Q82em4 streptomyc	805	23	100.0	297	2	P17437	P17437 mycobacteri
733	23	100.0	276	2	Q87LZ6	Q87lz6 vibrio para	806	23	100.0	297	2	Q746H2	Q746h2 thermus the
734	23	100.0	276	2	Q8VON5	Q8von5 planococcus	807	23	100.0	297	2	Q7N6L9	Q7n6l9 photorhabdu
735	23	100.0	276	2	Q91R83	Q91r83 banana stre	808	23	100.0	297	2	Q7TYM5	Q7tym5 mycobacteri
736	23	100.0	277	1	HESA_PLEBO	F46037 plectonema	809	23	100.0	297	2	Q87VL2	Q87vl2 pseudomonas
737	23	100.0	277	2	Q934A2	Q934a2 haemophilus	810	23	100.0	297	2	Q6NY38	Q6ny38 brachydanio
738	23	100.0	277	2	Q760B5	Q760b5 uncultured	811	23	100.0	298	2	Q7QC95	Q7qc95 anopheles g
739	23	100.0	277	2	Q9F1J0	Q9f1j0 enterococcu	812	23	100.0	298	2	Q8HBP4	Q8hbp4 bos taurus
740	23	100.0	277	2	Q8YB42	Q8yb42 brucella me	813	23	100.0	298	2	Q8HC24	Q8hc24 bos taurus
741	23	100.0	277	2	Q80WM7	Q80wm7 mus musculu	814	23	100.0	298	2	Q7D0V9	Q7d0v9 agrobacteri
742	23	100.0	278	2	Q6AT60	Q6at60 cryza sativ	815	23	100.0	298	2	Q8YDJ8	Q8yjd8 brucella me
743	23	100.0	278	2	Q53937	Q53937 streptomyc	816	23	100.0	298	2	Q7PQO7	Q7pqo7 chromobact
744	23	100.0	278	2	Q8NZK9	Q8nzk9 streptococc	817	23	100.0	298	2	Q89HC5	Q89hc5 bradyrhizob
745	23	100.0	278	2	Q99YA4	Q99ya4 streptococc	818	23	100.0	298	2	Q8FUU5	Q8fuu5 brucella su
746	23	100.0	278	2	Q9A295	Q9a295 caulobacter	819	23	100.0	299	1	SPAH_ECOL6	P13431 escherichia
747	23	100.0	278	2	Q9KUB5	Q9kub5 vibrio chol	820	23	100.0	299	2	Q93LBI	Q93lbi bifidobacte
748	23	100.0	278	2	Q8K603	Q8k603 streptococc	821	23	100.0	299	2	Q46686	Q46686 escherichia
749	23	100.0	278	2	Q8BNV0	Q8bnv0 mus musculu	822	23	100.0	299	2	Q53298	Q53298 escherichia
750	23	100.0	279	2	Q8UHH6	Q8uhh6 agrobacteri	823	23	100.0	299	2	Q6Y3B0	Q6y3b0 geobacter p
751	23	100.0	279	2	Q9R167	Q9r167 streptomyc	824	23	100.0	300	1	ERG3 MYCTU	O50619 mycobacteri
752	23	100.0	280	2	Q8N171	Q8n171 homo sapien	825	23	100.0	300	2	Q986Y1	Q986y1 rhizobium l
753	23	100.0	281	2	Q7MYI2	Q7myi2 photorhabdu	826	23	100.0	301	2	Q6DHX2	Q6dxx2 homo sapien
754	23	100.0	281	2	Q8DMU0	Q8dmu0 synchococc	827	23	100.0	301	2	Q6A723	Q6a723 caenorhabdi
755	23	100.0	282	2	Q6MSH3	Q6msh3 corynebacte	828	23	100.0	301	2	Q65U69	Q65u69 manheimia
756	23	100.0	282	2	Q7DVA2	Q7dja2 porphytomon	829	23	100.0	301	2	Q8PDZ1	Q8pdz1 xanthomonas
757	23	100.0	282	2	Q9R2Q8	Q9r2q8 bacteroides	830	23	100.0	301	2	Q8PQV9	Q8pqv9 xanthomonas
758	23	100.0	282	2	Q9RHH2	Q9rhh2 porphytomon	831	23	100.0	301	2	Q7UA63	Q7ua63 synchococc
759	23	100.0	282	2	Q69952	Q69952 streptomyc	832	23	100.0	301	2	Q9KZP5	Q9kzp5 streptomyc
760	23	100.0	282	2	Q92PV6	Q92pv6 rhizobium m	833	23	100.0	302	2	Q8GM49	Q8gm49 zymomonas m
761	23	100.0	282	2	Q8BPS8	Q8bps8 mus musculu	834	23	100.0	302	2	Q8PF07	Q8pf07 xanthomonas

835	23	100.0	303	2	O84108	O84108 chlamydia t	908	23	100.0	319	2	Q9F1V0	Q9F1V0 flavobacter
836	23	100.0	303	2	O8BRJ3	O8brj3 mus musculus	909	23	100.0	319	2	Q59531	Q59531 mycobacteri
837	23	100.0	304	2	O8N9R4	O8n9r4 homo sapien	910	23	100.0	319	2	Q6NQ08	Q6nq08 rhodopseu
838	23	100.0	304	2	O6PK51	O6pk51 homo sapien	911	23	100.0	319	2	Q7WK04	Q7wk04 bordetella
839	23	100.0	304	2	O8LHB6	O8lhb6 oryza sativ	912	23	100.0	319	2	Q8JCY0	Q8jcy0 human immun
840	23	100.0	304	2	O9X195	O9x195 arabidopsis	913	23	100.0	320	2	Q8N4Q3	Q8n4q3 homo sapien
841	23	100.0	305	2	O16308	O16308 caenorhabdi	914	23	100.0	320	2	O8N7Q9	Q8n7q9 homo sapien
842	23	100.0	305	2	O8MXR6	O8mxr6 caenorhabdi	915	23	100.0	320	2	Q7PHJ6	Q7phj6 anopheles g
843	23	100.0	305	2	Q7QDQ6	Q7qdq6 anopheles g	916	23	100.0	320	2	O8SAX5	O8sax5 oryza sativ
844	23	100.0	305	2	O935V5	O935v5 streptomyc	917	23	100.0	320	2	O6PRC7	O6prc7 oryza sativ
845	23	100.0	305	2	Q9FW2	Q9fw2 pseudomonas	918	23	100.0	320	2	O8BGS9	O8bgs9 m mus muscu
846	23	100.0	305	2	O8KB19	O8kb19 chlorobium	919	23	100.0	320	2	Q9CSQ4	Q9csq4 mus musculu
847	23	100.0	305	2	O82J66	O82j66 streptomyc	920	23	100.0	321	2	O88PT6	O88pt6 pseudomonas
848	23	100.0	305	2	O9CSR2	O9csr2 mus musculu	921	23	100.0	321	2	O8JB55	O8jb55 human immun
849	23	100.0	306	2	O98CI1	O98ci1 rhizobium l	922	23	100.0	322	1	ARGI_PIG	ARGI_PIG
850	23	100.0	306	2	O7WD35	O7wd35 bordetella	923	23	100.0	322	1	ARGI_HUMAN	ARGI_HUMAN
851	23	100.0	307	1	PDX1_DEIRA	Pdx1 deino	924	23	100.0	322	1	MYDM_HUMAN	MYDM_HUMAN
852	23	100.0	308	1	HEM1_THEAC	Hem1 thermoplas	925	23	100.0	322	2	Q9S7P1	Q9s7p1 oryza sativ
853	23	100.0	308	2	O6ES50	O6es50 oryza sativ	926	23	100.0	322	2	Q57054	Q57054 synechocyst
854	23	100.0	308	2	O6M781	O6m781 corynebacte	927	23	100.0	322	2	Q79F82	Q79f82 synechocyst
855	23	100.0	308	2	O53301	O53301 mycobacteri	928	23	100.0	322	2	O8KFW1	O8kfw1 chlorobium
856	23	100.0	308	2	O8NSI0	O8nsi0 corynebacte	929	23	100.0	322	2	O88H91	O88h91 pseudomonas
857	23	100.0	308	2	O8YNY0	O8yny0 anabaena sp	930	23	100.0	323	1	ARGI_MOUSE	ARGI_MOUSE
858	23	100.0	308	2	O7TXA5	O7txa5 mycobacteri	931	23	100.0	323	1	ARGI_RAT	ARGI_RAT
859	23	100.0	308	2	O88JH3	O88jh3 pseudomonas	932	23	100.0	323	1	Q8VM94	Q8vm94 rhodococcus
860	23	100.0	309	2	O8DIP3	O8dip3 synechococc	933	23	100.0	323	2	Q59563	Q59563 mycobacteri
861	23	100.0	309	1	KHSE_STRCO	Khse streptomyce	934	23	100.0	323	2	O7TY20	O7ty20 mycobacteri
862	23	100.0	309	2	Q95XV7	Q95xv7 caenorhabdi	935	23	100.0	323	2	O6DIU5	O6diu5 xenopus tro
863	23	100.0	309	2	O9MT23	O9mt23 arabidopsis	936	23	100.0	323	2	Q7ZYM1	Q7zym1 xenopus lae
864	23	100.0	309	2	O9X7I8	O9x7i8 pseudomonas	937	23	100.0	324	1	PIX2_RAT	PIX2_RAT
865	23	100.0	310	2	O8N5E8	O8n5e8 homo sapien	938	23	100.0	324	2	Q6NEP1	Q6neb1 rhodopseu
866	23	100.0	310	2	O8XX39	O8xx39 caenorhabdi	939	23	100.0	324	2	O827E3	O827e3 streptomyc
867	23	100.0	310	2	O8YZN7	O8yzn7 anabaena sp	940	23	100.0	325	2	Q17402	Q17402 caenorhabdi
868	23	100.0	311	2	O8TSS5	O8tss5 methanosarc	941	23	100.0	325	2	Q55392	Q55392 synechocyst
869	23	100.0	311	2	O19257	O19257 caenorhabdi	942	23	100.0	325	2	Q9RUM8	Q9rum8 deinococcus
870	23	100.0	311	2	O7VM42	O7vm42 bordetella	943	23	100.0	325	2	O8R4R6	O8r4r6 mus musculu
871	23	100.0	311	2	O7W5J9	O7w5j9 bordetella	944	23	100.0	325	2	O68FY1	O68fy1 rattus norv
872	23	100.0	312	2	O9N591	O9n591 caenorhabdi	945	23	100.0	325	2	O9D7J2	O9d7j2 m mus muscu
873	23	100.0	312	2	O9FR72	O9fr72 hordeum spo	946	23	100.0	325	2	O6GNG2	O6gng2 xenopus lae
874	23	100.0	312	2	Q9FE73	Q9fe73 hordeum spo	947	23	100.0	326	1	GC2_HUMAN	GC2_HUMAN
875	23	100.0	312	2	Q9FE74	Q9fe74 hordeum spo	948	23	100.0	326	2	O8NPF5	O8nfh5 homo sapien
876	23	100.0	312	2	Q9FPF2	Q9fpf2 hordeum spo	949	23	100.0	326	2	O8TDJ1	O8tdj1 homo sapien
877	23	100.0	312	2	Q9FPF2	Q9fpf2 hordeum spo	950	23	100.0	326	2	Q7Y038	Q7y038 mangifera i
878	23	100.0	312	2	Q9FPF4	Q9fpf4 hordeum spo	951	23	100.0	326	2	O9EXB4	O9fxb4 arabidopsis
879	23	100.0	312	2	Q9FPF5	Q9fpf5 hordeum spo	952	23	100.0	326	2	O80FI5	O80fi5 goose hemor
880	23	100.0	312	2	F72585	F72585 synechocyst	953	23	100.0	326	2	O6IP56	O6ip56 xenopus tro
881	23	100.0	312	2	O8CHX9	O8chx9 mus musculu	954	23	100.0	326	2	Q6IP56	Q6ip56 xenopus lae
882	23	100.0	313	1	QYAM_BACSU	Q45910 bacillus su	955	23	100.0	326	2	Q98YL3	Q98yl3 human immun
883	23	100.0	313	2	O27528	O27528 methanobact	956	23	100.0	327	1	GC4_HUMAN	GC4_HUMAN
884	23	100.0	313	2	O67F56	O67f56 comamonas a	957	23	100.0	327	1	GN1L_HUMAN	GN1L_HUMAN
885	23	100.0	313	2	O6A7A8	O6a7a8 propionibac	958	23	100.0	327	2	Q9XTU5	Q9xtu5 caenorhabdi
886	23	100.0	313	2	O8DL64	O8dl64 synechococc	959	23	100.0	327	2	Q6GNA1	Q6gna1 xenopus lae
887	23	100.0	314	1	STO2_CABEL	Q19958 caenorhabdi	960	23	100.0	327	2	Q632F0	Q632f0 oncorhynch
888	23	100.0	314	2	O6SH15	O6sh15 uncultured	961	23	100.0	328	2	Q6NA51	Q6na51 rhodopseu
889	23	100.0	314	2	P71628	P71628 mycobacteri	962	23	100.0	329	2	Q7R3P4	Q7r3p4 giardia lam
890	23	100.0	314	2	O8YVW0	O8ymv0 anabaena sp	963	23	100.0	330	1	GC1_HUMAN	GC1_HUMAN
891	23	100.0	314	2	O6LKH0	O6lkh0 photobacter	964	23	100.0	330	2	Q7Q5R3	Q7q5r3 anopheles g
892	23	100.0	314	2	Q7TXS3	Q7txs3 mycobacteri	965	23	100.0	330	2	O02946	O02946 macaca mula
893	23	100.0	315	2	O8WSM5	O8wsms caenorhabdi	966	23	100.0	330	2	O02947	O02947 macaca mula
894	23	100.0	315	2	P74817	P74817 sphingomon	967	23	100.0	330	2	O19356	O19356 macaca mula
895	23	100.0	315	2	Q7CSM9	Q7csm9 agrobacteri	968	23	100.0	330	2	Q88N48	Q88n48 pseudomonas
896	23	100.0	316	1	ARGI_XENLA	P30759 xenopus lae	969	23	100.0	330	2	Q7ZY96	Q7zy96 xenopus lae
897	23	100.0	316	2	O8PVT1	O8pvt1 methanosarc	970	23	100.0	331	2	O02944	O02944 macaca mula
898	23	100.0	316	2	O6LJV2	O6ljv2 photobacter	971	23	100.0	331	2	O02945	O02945 macaca mula
899	23	100.0	317	2	Q7R784	Q7r784 plasmodium	972	23	100.0	331	2	O8RTX8	O8rtx8 uncultured
900	23	100.0	317	2	O63LT9	O63lt9 burkholderi	973	23	100.0	332	2	O860F7	O860f7 macaca neme
901	23	100.0	317	2	O50655	O50655 mycobacteri	974	23	100.0	332	2	O860F8	O860f8 macaca neme
902	23	100.0	317	2	O7TWG4	O7twg4 mycobacteri	975	23	100.0	332	2	Q73W34	Q73w34 mycobacteri
903	23	100.0	317	2	O826F4	O826f4 streptomyc	976	23	100.0	332	2	Q8D8K6	Q8d8k6 vibrio vuln
904	23	100.0	318	2	O86YC0	O86yc0 homo sapien	977	23	100.0	332	2	Q7ZLU7	Q7zlu7 human immun
905	23	100.0	318	2	Q7NET6	Q7net6 gloebacter	978	23	100.0	333	2	Q92XES	Q92xes rhizobium m
906	23	100.0	319	1	TCB1_RABIT	P06333 oryctolagus	979	23	100.0	334	1	DUS2_SYNY3	P72872 synechocyst
907	23	100.0	319	2	Q59553	Q59553 mycobacteri	980	23	100.0	334	1	SCRE_KLEPN	P37076 klebsiella

981 23 100.0 334 2 Q6PRD4
 982 23 100.0 334 2 Q6ZAR5
 983 23 100.0 335 1 HEMZ MYCAV
 984 23 100.0 335 2 Q8MXF3
 985 23 100.0 335 2 Q9XTU3
 986 23 100.0 335 2 Q88QX5
 987 23 100.0 335 2 Q9CNK2
 988 23 100.0 335 2 Q9KSJ0
 989 23 100.0 335 2 Q9RGU4
 990 23 100.0 335 2 Q9CX85
 991 23 100.0 335 2 Q98YGA
 992 23 100.0 336 2 Q8IXR7
 993 23 100.0 336 2 Q8WSM6
 994 23 100.0 336 2 Q7DSH6
 995 23 100.0 336 2 Q64MY9
 996 23 100.0 336 2 Q7U7E6
 997 23 100.0 336 2 Q89VM0
 998 23 100.0 336 2 Q8A3W7
 999 23 100.0 336 2 Q8CVB9
 1000 23 100.0 336 2 Q6GLH2

ALIGNMENTS

RESULT 1
 Q91HB7 PRELIMINARY; PRT; 30 AA.
 AC Q91HB7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF2 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; Anellovirus.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bagaglia S., Morsica G., Sitia G.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY035368; AAK77020.1; -
 FT NON TER 30 30
 SQ SEQUENCE 30 AA; 3180 MW; 87EF45FB63BF7D15 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 16 GQPR 19

RESULT 2
 Q8VJ21 PRELIMINARY; PRT; 31 AA.
 AC Q8VJ21;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=WT3449.2;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RI DOI=10.1128/JB.184.19.5479-5490.2002;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
 RA Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL J. Bacteriol. 184:5479-5490 (2002).
 DR EMBL; AF000516; AAK47793.1; -
 DR TIGR; WT3449.2; -
 KW Hypothetical protein.
 SQ SEQUENCE 31 AA; 3532 MW; 7AB847CE65D3449 CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 11 GQPR 14

RESULT 3
 O06618 PRELIMINARY; PRT; 34 AA.
 AC O06618;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=Rv1572c;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C.M.,
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
 RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
 RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544 (1998).
 DR EMBL; BX842577; CAB09065.2; -
 DR Tuberculist; Rv1572c; -
 KW Complete proteome.
 SQ SEQUENCE 34 AA; 4005 MW; 2DCC9C17846AA537 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 9 GQPR 12

RESULT 4
 Q7TZW6 PRELIMINARY; PRT; 34 AA.
 AC Q7TZW6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein Mb1598A.
 GN Name=Mb1598A; ORFNames=Mb1598A;
 OS Mycobacterium bovis.

```

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
KW Complete proteome; Hypothetical protein.
DR EMBL; BX248339; CAD96266.1;
SQ SEQUENCE 34 AA; 4005 MW; 2DC9C17846AA537 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 9 GQPR 12

RESULT 5
Q679Y6 PRELIMINARY; PRT; 35 AA.
AC Q679Y6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mitochondrial DNA polymerase (Fragment).
GN Name=POLG;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Rovio A.T., Jacobs H.T.;
RT "PolyQ of POLG in Primates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV376482; AAR26639.1;
FT NON_TER 1 1
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 4062 MW; DE88831E291285E4 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 30 GQPR 33

RESULT 6
Q679Y8 PRELIMINARY; PRT; 36 AA.
AC Q679Y8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mitochondrial DNA polymerase (Fragment).
GN Name=POLG;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.

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RA Rovio A.T., Jacobs H.T.;
RT "PolyQ of POLG in Primates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV376480; AAR26637.1;
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4219 MW; A82FEAD61CS86C3 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 31 GQPR 34

RESULT 7
Q9UEU6 PRELIMINARY; PRT; 39 AA.
AC Q9UEU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Autosomal dominant polycystic kidney disease type II protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96207227; PubMed=8619474; DOI=10.1006/abio.1996.0138;
RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97264341; PubMed=9110174;
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
RT "Large-scale concatenation cDNA sequencing.";
RL Genome Res. 7:353-358(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF054992; AAC09351.1;
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 3837 MW; E4B4FE1DF07DIAD5 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 8 GQPR 11

RESULT 8
IM9A RAT STANDARD; PRT; 43 AA.
AC Q9WV37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM9 A (Fragment).
DE (Fragment).

```


GN Name=Timm9; Synonyms=Tim9a, Timm9a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer M.P., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
finger proteins involved in mitochondrial carrier import.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
similarity).
CC -!- SIMILARITY: Belongs to the Tim8/Tim10 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF150102; AAD40008.1; ALT TERM.
KW Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
FT NON_TER 1 1
SQ SEQUENCE 43 AA; 5003 MW; 462223C352F4168A7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 40 GQPR 43

RESULT 9
Q6WZF9 PRELIMINARY; PRT; 52 AA.
ID Q6WZF9
AC Q6WZF9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686J11229 (Fragment).
GN Name=DKF2p686J11229;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Human small intestine;
RC The German Human cDNA Consortium;
RG Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647062; CAE46080.1; -.
KW Hypothetical protein.
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5516 MW; B67A9A9DDFDEBE25 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 38 GQPR 41

RESULT 10

Q71V32 PRELIMINARY; PRT; 59 AA.
ID Q71V32
AC Q71V32
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mevalonate pyrophosphate decarboxylase (Fragment).
GN Name=Mvpd;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato N., Ueno K., Sawamura M., Nabika T., Yamori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036709; AAB92551.1; -.
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6674 MW; 8B6353329B34DDCF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 13 GQPR 16

RESULT 11
Q54820 PRELIMINARY; PRT; 61 AA.
ID Q54820
AC Q54820
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dnm protein.
GN Name=dnm;
OS Streptomyces peucetius.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97086506; PubMed=8932700;
RA Gallo M.A., Ward J., Hutchinson C.R.;
RT "The dnm gene in Streptomyces peucetius contains a naturally
occurring frameshift mutation that is suppressed by another locus
outside of the daunorubicin-production gene cluster.";
RL Microbiology 142:0-0(0).
DR EMBL; L47163; AAB50924.1; -.
SQ SEQUENCE 61 AA; 6572 MW; AD0A0E3DCE1F3F5A CRC64;

Query Match 100.0%; Score 23; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 45 GQPR 48

RESULT 12
Q6BWM8 PRELIMINARY; PRT; 62 AA.
ID Q6BWM8
AC Q6BWM8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome B of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0B10318g;

OS Debaryomyces hansenii CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxID=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer E., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Keraat A., Koszul R., Lemaite M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP STRAIN=CBS767;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382134; CAG85395.1; -.
 SQ SEQUENCE 62 AA; 7118 MW; 57F173A0FA111B2B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 24 GQPR 27

RESULT 13
 Q8U521 ID Q8U521 PRELIMINARY; PRT; 63 AA.
 AC Q8U521;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE AGR L 18p.
 GN OrderedLocusNames=AGR L 18;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cereon;
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Houello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Clelo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58";
 RL Science 294:2323-2328(2001).
 DR EMBL; AE008198; AAK88560.1; -.
 DR PIR; F98129; F98129.
 SQ SEQUENCE 63 AA; 7143 MW; 3410B4C7C9BC69BA CRC64;

Query Match 100.0%; Score 23; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 9 GQPR 12

RESULT 14
 Q8YMW9 ID Q8YMW9 PRELIMINARY; PRT; 65 AA.
 AC Q8YMW9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Asl4805 protein.
 GN OrderedLocusNames=asl4805;
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003597; BAB76504.1; -.
 DR PIR; AE2406; AE2406.
 KW Complete proteome.
 SQ SEQUENCE 65 AA; 7215 MW; E397D308DA33AC44 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 27 GQPR 30

RESULT 15
 Q9K880 ID Q9K880 PRELIMINARY; PRT; 67 AA.
 AC Q9K880;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE BH3126 protein.
 GN OrderedLocusNames=BH3126;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001517; BAB06845.1; -.
 DR PIR; F84040; F84040.
 DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro; IPR001455; SIRA_like.
 KW Complete proteome.
 SQ SEQUENCE 67 AA; 7735 MW; 0825029A4C8FBC4E CRC64;

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 58 GQPR 61

RESULT 16

Q7UWU3 PRELIMINARY; PRT; 72 AA.
 AC Q7UWU3
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB1787;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294135; CAD72269.1; --
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 72 AA; 8185 MW; 21E56AE94AF1337C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 47 GQPR 50

RESULT 17

Q7PFF50 PRELIMINARY; PRT; 73 AA.
 AC Q7PFF50
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE ENSANGP0000022726 (Fragment).
 GN Name=ENSANGG0000021610;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008807; EAA45464.1; --
 FT NON TER 1
 SQ SEQUENCE 73 AA; 7734 MW; 5DA167D728A8C629 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 46 GQPR 49

RESULT 18

Q6A863 PRELIMINARY; PRT; 73 AA.
 AC Q6A863
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PPA1303;
 OS Propionibacterium acnes.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
 OX NCBI_TaxID=1747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KPA171202 / DSM 16379;
 RX PubMed=15286373; DOI=10.1126/science.1100330;
 RA Brueggemann H., Henne A., Hoster F., Liesegang H., Wierer A.,
 RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
 RT "The complete genome sequence of Propionibacterium acnes, a commensal
 RT of human skin.";
 RL Science 305:671-673 (2004).
 DR EMBL; AS017283; AAT83052.1; --
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 73 AA; 7703 MW; 6BDAE2B358897DEE CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 52 GQPR 55

RESULT 19

Q80W36 PRELIMINARY; PRT; 73 AA.
 AC Q80W36
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b,
 DE isoform 1.
 GN Name=Atp5f1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RL ENBL; BC049640; AAH49640.1; -

DR MGB; MGI:1100495; Atp5f1.

DR GO; GO:0005739; C:mitochondrion; IDA.

DR InterPro; IPR008688; Mt_ATP-synth_B.

DR Pfam; PF05405; Mt_ATP-synt_B; 1.

SQ SEQUENCE 73 AA; 7703 MW; 8D05D748E6292FBE CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

DB 37 GQPR 40

RESULT 20

Q7V8P7 ID Q7V8P7 PRELIMINARY; PRT; 74 AA.

AC Q7V8P7;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical.

GN OrderedLocusNames=PMW0288;

OS Prochlorococcus marinus (strain MIT 9313).

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;

OC Prochlorococcus

OX NCBI_TaxID=74547;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,

RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,

RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

RA Webb E.A., Zinser E.R., Chisholm S.W.;

RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic

RT niche differentiation.";

RL Nature 424:1042-1047(2003).

RL ENBL; BX572095; CAE20463.1; -

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 74 AA; 7920 MW; 37D987F91F33C9F1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

DB 55 GQPR 58

RESULT 21

Q8DH17

ID Q8DH17 PRELIMINARY; PRT; 75 AA.

AC Q8DH17;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Tel1972 protein.

GN OrderedLocusNames=tsl1972;

OS Synechococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32046;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BP-1;
 RC MEDLINE=22225144; PubMed=12240834;
 RX Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Nakazaki N.,
 RA Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the thermophilic cyanobacterium
 RT Thermosynechococcus elongatus BP-1.";
 RL DNA Res. 9:123-130(2002).
 RL ENBL; AP005375; BAC09524.1; -
 KW Complete proteome.
 SQ SEQUENCE 75 AA; 8106 MW; 91EDBB412CEE1B1C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

DB 27 GQPR 30

RESULT 22

Q6TLY2 ID Q6TLY2 PRELIMINARY; PRT; 76 AA.

AC Q6TLY2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Ketosynthase (fragment).

OS Streptomyces hygroscopicus.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1912;

RN [1]

RP SEQUENCE FROM N.A.

RA Ayuso A., Genilloud O.;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AV394458; AAR01271.1; -

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0006833; P:fatty acid biosynthesis; IEA.

DR InterPro; IPR000794; Ketoacyl synth.

DR Pfam; PF02801; Ketoacyl-synt_C; 1.

FT NON_TER 1 1

FT NON_TER 76 76

SQ SEQUENCE 76 AA; 7978 MW; B4593E57C280E8BF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

DB 61 GQPR 64

RESULT 23

Q7R5L8

ID Q7R5L8 PRELIMINARY; PRT; 77 AA.

AC Q7R5L8;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE GUP_487_7109570862.

OS Giardia lamblia ATCC 50803.

OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.

OX NCBI_TaxID=184922;

RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000004; EAA42624.1; -.
SQ SEQUENCE 77 AA; 8263 MW; ADAF8BC487DC40AD CRC64;

Query Match 100.0%; Score 23; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 51 GQPR 54

RESULT 24
Q6ESF6 PRELIMINARY; PRT; 81 AA.
ID Q6ESF6
AC Q6ESF6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0605D08.19.
GN Names=P0605D08.19;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005110; BAD28414.1; -.
KW Hypothetical protein.
SQ SEQUENCE 81 AA; 8367 MW; 7AFC9E7C4992B349 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 77 GQPR 80

RESULT 25
Q8P835 PRELIMINARY; PRT; 81 AA.
ID Q8P835
AC Q8P835;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DE Sarcosine oxidase alpha subunit.
GN Names=socX; OrderedLocusNames=XCC2413;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,

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RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AS012352; AM41691.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001041; Ferredoxin.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8559 MW; 0A68118C1BBA718D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 39 GQPR 42

RESULT 26
Q72CR2 PRELIMINARY; PRT; 81 AA.
ID Q72CR2
AC Q72CR2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DVU1221;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AS017313; AAS95699.1; -.
DR TIGR; DVU1221; -.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8857 MW; 964517E2E58D9E54 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 31 GQPR 34

RESULT 27
Q96Q33

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ID Q96Q33 PRELIMINARY; PRT; 82 AA.
AC Q96Q33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ALS2CR14 protein.
GN Name=ALS2CR14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21470351; PubMed=11586298; DOI=10.1038/ngl001-166;
RA Hadano S., Hand C.K., Osuga H., Yanagisawa Y., Ootomo A., Devon R.S.,
RA Miyamoto N., Showguchi-Miyata J., Okada Y., Singaraja R.,
RA Figlewicz D.A., Kwiatkowski T., Hosler B.A., Sagie T., Skaug J.,
RA Nasir J., Brown R.H., Jr, Scherer S.W., Rouleau G.A., Hayden M.R.,
RA Ikeda J.-E.;
RT "A gene encoding a novel GTPase regulator is mutated in familial
RT amyotrophic lateral sclerosis 2.";
RL Nat. Genet. 29:166-173(2001).
DR EMBL; AB053316; BAB9024.1; -.
DR Genew; HGNC:14441; ALS2CR14.
DR InterPro; IPR010504; Arfaptin.
DR Pfam; PF06456; Arfaptin; 1.
DR PROSITE; PS00870; AH; 1.
SQ SEQUENCE 82 AA; 9599 MW; 77B0D7E497517FEF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 5 GQPR 8

RESULT 28
Q9X5W4 PRELIMINARY; PRT; 82 AA.
AC Q9X5W4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MoaD.
GN Name=moaD;
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=37b4;
RA Solomon P.S., Shaw A.L., McEwan A.G.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF128444; AAD21202.1; -.
DR HSP; P30748; IJW9.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; MoaD.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMs; TIGR01682; moaD; 1.
SQ SEQUENCE 82 AA; 8895 MW; A97135C7BCC2AA17 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

us-10-731-921-3.rup

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RESULT 29
Q86TT0 PRELIMINARY; PRT; 85 AA.
AC Q86TT0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Full-length cDNA clone CS0DC020YC12 of Neuroblastoma of Homo sapiens
DE (human)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Genoscope;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX161407; CAD61886.1; -.
SQ SEQUENCE 85 AA; 9314 MW; BD506B062C499167 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 58 GQPR 61

RESULT 30
Q8S0W2 PRELIMINARY; PRT; 85 AA.
AC Q8S0W2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE QJ1014 G12.12 protein.
GN Name=QJ1014_G12.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuuchi N., Kono I.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kamiya K.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakaehima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terashima K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF003372; BAB89078.1; -.
DR Gramene; Q8S0W2; -.
SQ SEQUENCE 85 AA; 9060 MW; 6B20E85090EFAE3F CRC64;

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Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 16 GQPR 19

RESULT 31
Q856X1 PRELIMINARY; PRT; 86 AA.
AC Q856X1
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp63.
OS Mycobacteriophage Rosebush.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205874;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.B., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AY129334; ANA01905.1; -
SQ SEQUENCE 86 AA; 9533 MW; 6E7BB1F300737C5C CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 6 GQPR 9

RESULT 32
Q8WZ93 PRELIMINARY; PRT; 87 AA.
AC Q8WZ93
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE NAG11.
GN Name=NAG11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nasopharyngeal epithelium;
RA Yu Y., Li G.Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170307; AAL35407.1; -
SQ SEQUENCE 87 AA; 9840 MW; 5EDA46F2A7D6524E CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 53 GQPR 56

RESULT 33
Q7U442 PRELIMINARY; PRT; 87 AA.
AC Q7U442
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocusNames=SYNW2233;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.B., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569695; CAE08748.1; -
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 69 87 Potential.
SQ SEQUENCE 87 AA; 9597 MW; 9E9CE7ACCB35960B CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 39 GQPR 42

RESULT 34
GVPB_BACME STANDARD; PRT; 88 AA.
AC G68677;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gas vesicle structural protein B (GVP B).
GN Name=gvpB;
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VT1660;
RX MEDLINE=98233742; PubMed=9573198;
RA Li N., Cannon M.C.;
RT "Gas vesicle genes identified in Bacillus megaterium and functional
expression in Escherichia coli.";
RL J. Bacteriol. 180:2450-2458(1998).
CC -I- FUNCTION: Gas vesicles are small, hollow, gas filled protein
structures that are found in several microbial planktonic
microorganisms. They allow the positioning of the organism at the
favorable depth for growth. GvpA type proteins form the essential
core of the structure.
CC -I- SUBCELLULAR LOCATION: Gas vesicle membrane.
CC -I- SIMILARITY: Belongs to the gas vesicle protein type A family.
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CC -----
CC EMBL; AF053765; AAC38416.1; -
CC HAWAP; MF_00576; -; 1.
CC InterPro; IPR000638; Gas_vesicle.
CC Pfam; PF00741; Gas_vesicle; 1.
CC -----
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DR ProDom; PD003598; Gas_vesicle; 1.
DR PROSITE; PS00234; GAS_VESICLE_A.1; 1.
DR PROSITE; PS00669; GAS_VESICLE_A.2; 1.
KW Gas vesicle.
SQ SEQUENCE 88 AA; 9618 MW; 5F089DE77358D84A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. NO. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 82 GQPR 85

RESULT 35
IM9A_HUMAN
ID _IM9A_HUMAN STANDARD; PRT; 89 AA.
AC Q9Y5J7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM9 A.
GN Names=TIM9; Synonyms=TIM9A, TIM9A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20021763; PubMed=10552927; DOI=10.1006/geno.1999.5966;
RA Jin H., Kendall E., Freeman T.C., Roberts R.G., Vetric D.L.;
RT "The human family of deafness/dystonia peptide (DDP) related
RL mitochondrial import proteins.";
RL Genomics 61:259-267(1999).
RN [2]
SEQUENCE FROM N.A.
RP Bauer M.F., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
RT finger proteins involved in mitochondrial carrier import.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Likely to be involved in the import and insertion of
CC hydrophobic membrane proteins into the mitochondrial inner
CC membrane.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Ubiquitous, with highest expression in heart,
CC kidney, liver and skeletal muscle.
CC -!- SIMILARITY: Belongs to the Tim8/Tim10 family.

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CC -----
DR EMBL; AF152353; AAF15103.1; -
DR EMBL; AF150100; AAD40006.1; -
DR EMBL; BC020213; AAH20213.1; -
DR EMBL; BC054875; AAH54875.1; -
DR PIR; T51191; T51191.
DR Genew; HGNC:11819; TIMM9.
DR MIM; 607384; -
DR GO; GO:0005744; C:mitochondrial inner membrane presequence tr. . .; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0007605; P:protein-mitochondrial targeting; TAS.
DR GO; GO:0006626; P:piprotein-mitochondrial targeting; TAS.
DR InterPro; IPR004217; Znf.Tim10/DDP.
DR Pfam; PF02953; zf-Tim10/DDP; 1.
KW Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
SQ SEQUENCE 89 AA; 10378 MW; 00F17CF6332ABF48 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. NO. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 86 GQPR 89

RESULT 36
IM9A_MOUSE
ID _IM9A_MOUSE STANDARD; PRT; 89 AA.
AC Q9WV98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM9 A.
GN Names=Timm9; Synonyms=Tim9a, Timm9a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP Bauer M.F., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
RT finger proteins involved in mitochondrial carrier import.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,

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RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Tim8/Tim10 family.
CC -----
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CC -----
CC EMBL; AF150101; AAD40007.1; -.
CC EMBL; AK018764; BAB31394.1; -.
CC EMBL; BC024370; AAH24370.1; -.
CC PIR; T51192; T51192.
CC MGD; MGI:1353432; Timm9.
CC InterPro; IPR004217; Znf_Tim10/DDP.
CC Pfam; PF02953; znf-Tim10/DDP; 1.
KW Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
SQ SEQUENCE 89 AA; 10344 MW; 1A40D7F491A09548 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 86 GQPR 89
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RESULT 37
Q68V99 PRELIMINARY; PRT; 89 AA.
ID Q68V99
RT "Phylogenetic position of the Diadromus pulchellus ascovirus DNA
RT polymerase among viruses with large double-stranded DNA genomes.";
RL J. Gen. Virol. 81:3059-3072 (2000).
DR EMBL; AJ279813; CAC19137.1; -.
DR InterPro; IPR003439; ABC transporter.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 89 AA; 9743 MW; EEFEPF817BCF22BCE CRC64;
Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 27 GQPR 30
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RESULT 39
HYPC_ECOLI STANDARD; PRT; 90 AA.
ID HYPC_ECOLI
AC P24191;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
```

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AC O68V99;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative methane monooxygenase, alpha subunit (fragment).
GN Names=pmoA;
OS uncultured methanotrophic bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=288814;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolb S., Knief C., Dunfield P., Conrad R.;
RT "Abundance and activity of uncultured methanotrophic bacteria involved
RT in consumption of atmospheric methane in two forest soils.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ786669; CAH10419.1; -.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR InterPro; IPR005829; Sug transporter.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW Monooxygenase.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 9839 MW; 8A70CB602A043513 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 7 GQPR 10
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RESULT 38
Q9DSU8 PRELIMINARY; PRT; 89 AA.
ID Q9DSU8
AC Q9DSU8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Ascovirus DpAV4.
OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
OX NCBI_TaxID=113365;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540044; PubMed=11086137;
RA Stasiak K., Demattai M.V., Federici B.A., Bigot Y.;
RT "Phylogenetic position of the Diadromus pulchellus ascovirus DNA
RT polymerase among viruses with large double-stranded DNA genomes.";
RL J. Gen. Virol. 81:3059-3072 (2000).
DR EMBL; AJ279813; CAC19137.1; -.
DR InterPro; IPR003439; ABC transporter.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 89 AA; 9743 MW; EEFEPF817BCF22BCE CRC64;
Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 27 GQPR 30
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DE Hydrogenase isoenzymes formation protein hypc.
GN Name=hypc;
GN OrderedLocusNames=b2728, c3288, z4037, ECs3584, SF2745, S2937;
OS Escherichia coli, O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA MEDLINE=91194542; PubMed=1849603;
RX Lutz S., Jacobi A., Schlensog V., Boehm R., Sawers G., Boeck A.;
RT "Molecular characterization of an operon (hyp) necessary for the
RT activity of the three hydrogenase isoenzymes in Escherichia coli.";
RL Mol. Microbiol. 5:123-135(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=11206551; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441 (2002).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
RN [9]
RP POSSIBLE FUNCTION.
RC SPECIES=E.coli;
RX MEDLINE=98153119; PubMed=9485446; DOI=10.1021/b19720078;
RA Drapal N., Boeck A.;
RT "Interaction of the hydrogenase accessory protein HypC with HycE, the
RT large subunit of Escherichia coli hydrogenase 3 during enzyme
RT maturation.";
RL Biochemistry 37:2941-2948(1998).
CC -!- FUNCTION: Is required for the formation of all three hydrogenase
CC isoenzymes. May bind to the precursor form of the large subunit of
CC dehydrogenases to keep them in a conformation accessible for metal
CC incorporation.
CC -!- SIMILARITY: Belongs to the hypE/hypC family.
CC
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CC
CC EMBL; X54543; CAA38414.1; -;
CC EMBL; U29579; AAA69238.1; -;
CC EMBL; U00096; AAC75770.1; -;
CC EMBL; A5016765; AAN81737.1; -;
CC EMBL; AP005501; AAG57836.1; -;
CC EMBL; AP002562; BAB37007.1; -;
CC EMBL; A5015289; AAN44236.1; -;
CC EMBL; A5016987; AAP18063.1; -;
CC PIR; H85921; H85921.
CC PIR; H91076; H91076.
CC PIR; S15199; S15199.
CC ECO2DBASE; A008.0; 6TH EDITION.
CC ECHOBASE; EB0480; -;
CC EcoGene; EG10485; hypC.
CC InterPro; IPR001109; HypE_HypC.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC Pfam; PF01455; HypE_HypC; 1.
CC PIRSF; PIRSF005618; HypE_HypC; 1.
CC PRINTS; PR00445; HUPFHYPC.
CC ProDom; PD003112; HypE_HypC; 1.
CC TIGRFAMs; TIGR00074; hypC_hupF; 1.
CC PROSITE; PS01097; HUPF_HYPYC; 1.
CC Complete proteome.
CC
CC SQ SEQUENCE 90 AA; 9732 MW; FBE252F1875C7879 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : 1 GQPR 4
Db 40 GQPR 43

RESULT 40
QBXG01 PRELIMINARY; PRT; 90 AA.
ID QBXG01

AC Q8XG01; Q7AMES;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hydrogenase isoenzymes formation protein hupF.
 GN Name=hupF; OrderedLocusNames=STY2978, t2758;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RC MEDLINE=21534947; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyfanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor T.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feilwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR ENBL; AE016843; AA070319.1; -;
 DR ENBL; AL627276; CAD05963.1; -;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR PFam; PF01455; HupF_HyPC; 1.
 DR PIRSF; PIRSF005618; HupF_HyPC; 1.
 DR PRINTS; PR00445; HUPFHYP; 1.
 DR PRODom; PD003112; HupF_HyPC; 1.
 DR TIGRFAMs; TIGR00074; hupF_hupF; 1.
 DR PROSITE; PS01097; HUPF_HYPC; 1.
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 9744 MW; 6D1F99EB36EC6555 CRC64;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RC MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor T.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feilwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR ENBL; AE016843; AA070319.1; -;
 DR ENBL; AL627276; CAD05963.1; -;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR PFam; PF01455; HupF_HyPC; 1.
 DR PIRSF; PIRSF005618; HupF_HyPC; 1.
 DR PRINTS; PR00445; HUPFHYP; 1.
 DR PRODom; PD003112; HupF_HyPC; 1.
 DR TIGRFAMs; TIGR00074; hupF_hupF; 1.
 DR PROSITE; PS01097; HUPF_HYPC; 1.
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 9744 MW; 6D1F99EB36EC6555 CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 40 GQPR 43

RESULT 41

ID Q7CPX9 PRELIMINARY; PRT; 90 AA.
 AC Q7CPX9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative hydrogenase expression/formation protein.
 GN Name=hupF; OrderedLocusNames=STW2856;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RC MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 Query Match 100.0%; Score 23; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 75 GQPR 78

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AS008830; AAL21736.1; -;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001109; HupF_HyPC.
 DR InterPro; IPR008994; Nucleic acid_OB.
 DR PFam; PF01455; HupF_HyPC; 1.
 DR PIRSF; PIRSF005618; HupF_HyPC; 1.
 DR PRINTS; PR00445; HUPFHYP; 1.
 DR PRODom; PD003112; HupF_HyPC; 1.
 DR TIGRFAMs; TIGR00074; hupF_hupF; 1.
 DR PROSITE; PS01097; HUPF_HYPC; 1.
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 9744 MW; 6D1F99EB36EC6555 CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 40 GQPR 43

RESULT 42

ID Q7W0F6 PRELIMINARY; PRT; 90 AA.
 AC Q7W0F6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative exported protein.
 GN OrderedLocusNames=BP0181;
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
 RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feilwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640411; CAE40560.1; -;
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 9780 MW; 30CA43B5FD67A8B3 CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB 75 GQPR 78

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RESULT 43
Q7W1D7 PRELIMINARY; PRT; 90 AA.
AC Q7W1D7;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Putative exported protein.
GN OrderedLocusNames=BPP0756;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640425; CAB40165.1; -.
KW Complete proteome.
SQ SEQUENCE 90 AA; 9812 MW; 30DE13B5FD67A8B3 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 75 GQPR 78

RESULT 44
Q7WP44 PRELIMINARY; PRT; 90 AA.
AC Q7WP44;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Putative exported protein.
GN OrderedLocusNames=BB0841;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).

RESULT 45
Q8YRZ8 PRELIMINARY; PRT; 91 AA.
AC Q8YRZ8;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Aar3294 protein.
GN OrderedLocusNames=aar3294;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Iehikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003592; BAB74993.1; -.
DR PIR; AG2217; AG2217.
DR GO; GO:0006790; P; sulfur metabolism; IEA.
DR Pfam; PF02597; This; 1.
KW Complete proteome.
SQ SEQUENCE 91 AA; 9679 MW; 93965078BD48EEF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 51 GQPR 54

RESULT 46
Q84VP6 PRELIMINARY; PRT; 92 AA.
AC Q84VP6;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein At5g21110.
GN Names=At5g21110;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning C.M.,
RA Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken S.E.,
RA Feldblum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC140977; AAC073885.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10268 MW; 9229E7FCBEFF144F CRC64;

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 14 GQPR 17

RESULT 47
Q91UP6 PRELIMINARY; PRT; 94 AA.
AC Q91UP6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Plasmid PSB102.
OG Plasmid PSB102.
OC other sequences; broad host range plasmids.
OX NCBI_TaxID=146518;
RN [1]
RA Schaefer S., Keller M., Droegge M., Lanka E., Puehler A.,
RA selbitschka W.;
RT "The genetic organization and evolution of the broad-host-range
RT mercury resistance plasmid PSB102 isolated from a microbial population
RT residing in the rhizosphere of alfalfa.";
RL Nucleic Acids Res. 29:5169-5181(2001).
DR EMBL: AJ304453; CAC79191.1; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 94 AA; 10338 MW; 3DB2F5265FF12C84 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 50 GQPR 53

RESULT 48
Q8SA29 PRELIMINARY; PRT; 95 AA.
AC Q8SA29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P0684E06.15 protein (P0445H04.6 protein).
GN Names=P0684E06.15; Synonyms=P0445H04.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machata K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaoka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata K.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

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RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL: AF003291; BAB85269.1; -
DR EMBL: AF004364; BAC06295.1; -
DR Gramene; Q8SA29; -
SQ SEQUENCE 95 AA; 10364 MW; 92507AEF0533E2F0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 16 GQPR 19

RESULT 49
Q9F6C4 PRELIMINARY; PRT; 96 AA.
AC Q9F6C4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Propionicin Tl.
GN Name=pctA;
OS Propionibacterium thoenii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1751;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20466828; PubMed=11010864;
RX DOI=10.1128/AEM.66.10.4230-4236.2000;
RA Faye T., Langsrud T., Nes I.F., Holo H.;
RT "Biochemical and genetic characterization of propionicin Tl, a new
RT bacteriocin from Propionibacterium thoenii.";
RL Appl. Environ. Microbiol. 66:4230-4236(2000).
DR EMBL: AF294258; AAG24829.1; -
SQ SEQUENCE 96 AA; 10045 MW; ED11F314D1C78F8 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 86 GQPR 89

RESULT 50
Q9YCI1 PRELIMINARY; PRT; 98 AA.
AC Q9YCI1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APES047.
GN ORFNames=APES047;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

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RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR ENBL; AP000061; BAA80266.1; -.
 DR PIR; D72601; D72601.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 98 AA; 10497 MW; C135B70F14DCC00B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 25 GQPR 28

RESULT 51

Q7QUD9 PRELIMINARY; PRT; 98 AA.
 AC Q7QUD9;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP 59 26262 25966.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.; Giardia lamblia genome.";
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR ENBL; AACB0100094; EAA38654.1; -.
 SQ SEQUENCE 98 AA; 10946 MW; DB918E4612BB26D1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 45 GQPR 48

RESULT 52

Q68QC8 PRELIMINARY; PRT; 99 AA.
 AC Q68QC8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Protease (Fragment).
 GN Name=pol;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodrigues R., Custodio R.M., Ferreira J.L.P., Oliveira C.M.,
 RA Franco H.M., Ferreira L.S.B., Brigido L.F.M.;
 RT "ARV Resistance Mutations in Non-B clades HIV-1.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AY643155; AAR96726.1; -.
 SQ SEQUENCE 99 AA; 10497 MW; 6DCA719E7FC94B1B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||

DR InterPro; IPR009007; Pept Aspartic.
 DR InterPro; IPR001969; Pept Asp_AS.
 DR Pfam; PF00077; RVP; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
 KW Protease.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10715 MW; 8E209C85F9271B20 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 17 GQPR 20

RESULT 53

Q9Q2H7 PRELIMINARY; PRT; 99 AA.
 AC Q9Q2H7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE V-1 protease (Fragment).
 GN Name=ORF;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21091889; PubMed=11181376;
 RA Servais J., Lambert C., Fontaine E., Plesseria J.M., Robert I.,
 RA Arendt V., Staub T., Schneider F., Hemmer R., Burtonboy G.,
 RA Schmit J.C.;
 RT "Variant human immunodeficiency virus type 1 proteases and response to
 RT combination therapy including a protease inhibitor.";
 RL Antimicrob. Agents Chemother. 45:893-900(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102417; PubMed=11158089;
 RA Servais J., Lambert C., Fontaine E., Plesseria J.M., Robert I.,
 RA Arendt V., Staub T., Schneider F., Hemmer R., Burtonboy G.,
 RA Schmit J.C.;
 RT "Comparison of DNA sequencing and a line probe assay for detection of
 RT human immunodeficiency virus Type 1 in patients failing highly active
 RT antiretroviral therapy.";
 RL J. Clin. Microbiol. 39:454-459(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Servais J.A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ279595; CAB66008.1; -.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0008508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001995; Peptidase A2.
 DR InterPro; IPR009007; Pept Aspartic.
 DR Pfam; PF00077; RVP; 1.
 DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
 KW Protease.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10829 MW; 6DCA719E7FC94B1B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||

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Db      17 GQPR 20
RESULT 54
Q90DC9 PRELIMINARY; PRT; 100 AA.
AC Q90DC9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=SIVsmSL92b;
RX MEDLINE=96211494; PubMed=8648696;
RA Chen Z., Telfier P., Gettie A., Reed P., Zhang L., Ho D.D., Marx P.A.;
RT "Genetic characterization of new West African simian immunodeficiency
RT virus SIVsm: Geographic clustering of household-derived SIV strains
RT with human immunodeficiency virus type 2 subtypes and genetically
RT diverse viruses from a single feral sooty mangabey troop.";
RL J. Virol. 70:3617-3627(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SIVsmSL92b;
RX MEDLINE=21413368; PubMed=11522185; DOI=10.1089/088922201316912763;
RA Chakrabarti L.A., Luckay A., Marx P.A.;
RT "A divergent simian immunodeficiency virus from sooty mangabey with an
RT atypical Tat-TAR structure.";
RL AIDS Res. Hum. Retroviruses 17:1155-1165(2001).
DR EMBL; AF334679; AAK55278.1; -.
DR HSP; P12520; 1BDE.
DR PFam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
SQ SEQUENCE 100 AA; 11433 MW; A420DE62297D7C8B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 82 GQPR 85

-RESULT 55
Q7PJ39 PRELIMINARY; PRT; 101 AA.
AC Q7PJ39;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE ENSANGP0000024894.
GN Name=ENSANGG00000009298;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAA43910.1; -.
SQ SEQUENCE 101 AA; 11333 MW; CE6533E507EBE1E8 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 40 GQPR 43

RESULT 56
Q7G4Y8 PRELIMINARY; PRT; 101 AA.
AC Q7G4Y8;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OSJNB0011A24.34;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RC SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017063; AAP52397.1; -.
KW Hypothetical protein.
SQ SEQUENCE 101 AA; 10958 MW; DA57AD537DBC6603 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 36 GQPR 39

RESULT 57
Q88Q57 PRELIMINARY; PRT; 101 AA.
AC Q88Q57;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PP0641;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.;
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.N.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Fimmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
```

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RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AF061776; AAN66266.1; -.
DR TIGR; PP0641; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 101 AA; 11214 MW; AC09CL37CE55B2D9 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
10 GQPR 13

RESULT 58
Q9RWS5 PRELIMINARY; PRT; 101 AA.
AC Q9RWS5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR0590.
GN OrderedLocusNames=DR0590;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamatheva J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001917; AAF10172.1; -.
DR PIR; F75500; F75500.
DR TIGR; DR0590; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 101 AA; 10629 MW; 74B390E0E8A827DC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
54 GQPR 57

RESULT 59
Q8UEN1 PRELIMINARY; PRT; 101 AA.
AC Q8UEN1; Q7CYN7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein Atu1725 (AGR_C3166p).
GN OrderedLocusNames=AGR_C3166, Atu1725;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
45 GQPR 48

RESULT 60
Q79F64 PRELIMINARY; PRT; 102 AA.
AC Q79F64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RNA-binding protein.
GN Name=rbpA1;
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M3;
RX MEDLINE=94250845; PubMed=8193307;
RA Sato N.;
RT "A cold-regulated cyanobacterial gene cluster encodes RNA-binding
RT protein and ribosomal protein S21.";
RL Plant Mol. Biol. 24:819-823(1994).
DR EMBL; D17710; BAA04563.1; -.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; RRM 1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 102 AA; 10963 MW; BA565080DB222875 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
45 GQPR 48

MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009129; AAL42724.1; -.
DR EMBL; AE008094; AAK87496.1; -.
DR PIR; AF2788; AF2788.
DR PIR; G97567; G97567.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 101 AA; 11070 MW; 6E5B87180682BFC1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
45 GQPR 48

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 39 GQPR 42

RESULT 61
Q44560 PRELIMINARY; PRT; 102 AA.
AC Q44560;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA-binding protein.
GN Names:rbpA1; OrderedLocusNames=alr0741;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003583; BAB72698.1; .
DR PIR; AC1899; AC1899.
DR PIR; I39621; I39621.
DR HSP; P19339; 3SXL.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Complete proteome.
SQ SEQUENCE 102 AA; 10963 MW; BA565080DB222875 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 39 GQPR 42

RESULT 62
Q8CAG4 PRELIMINARY; PRT; 102 AA.
ID Q8CAG4
AC Q8CAG4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
DE library, clone:A230065N10 product:hypothetical protein, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

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SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishize T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AK038819; BAC30137.1; .
KW Hypothetical protein.
SQ SEQUENCE 102 AA; 10304 MW; BA9B3985529AEEF7 CRC64;

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Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 47 GQPR 50

RESULT 63
Q6Z289 PRELIMINARY; PRT; 103 AA.
ID Q6Z289
AC Q6Z289;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNBa0086F04.21.

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GN Names=OSUNB0086F04.21;
OS Oryza sativa (Japonica cultivar-group);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AP005388; BAC98679.1; -.
KW Hypochemical protein.
SQ SEQUENCE 103 AA; 11794 MW; 63F6CAD6D324C2B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 82 GQPR 85

RESULT 64
Q934X9 PRELIMINARY; PRT; 103 AA.
ID Q934X9
AC Q934X9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypochemical protein HCM2.0088C.
GN OrderedLocusNames=HCM2.0088C;
OS Salmonella typhi.
OG Plasmid pHCN2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR ENBL; AL513384; CAD09955.1; -.
KW Complete proteome; Hypochemical protein; Plasmid.
SQ SEQUENCE 103 AA; 11459 MW; 069BE3BE3A8B3324 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 12 GQPR 15

RESULT 65
Q6LV85 PRELIMINARY; PRT; 103 AA.
ID Q6LV85
AC Q6LV85;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical anti-anti-sigma regulatory factor.

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GN Names=VP1476; OrderedLocusNames=PBPR0351;
OS Photobacterium profundum (Photobacterium sp. (strain S89)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the anti-sigma-factor antagonist family.
CC -1- SIMILARITY: Contains 1 STAS domain.
DR ENBL; CR378664; CAG18790.1; -.
DR InterPro; IPR003658; Antisig_antgnst.
DR InterPro; IPR002645; STAS.
DR ProDom; PD005210; Antisig_antgnst; 1.
DR TIGRFAMs; TIGR00377; ant_ant_sig; 1.
DR PROSITE; PS50801; STAS; 1.
KW Complete proteome.
SQ SEQUENCE 103 AA; 11711 MW; 1CC195998E5D0EC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 79 GQPR 82

RESULT 66
Q9Q2P0 PRELIMINARY; PRT; 103 AA.
ID Q9Q2P0
AC Q9Q2P0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE RPS1 protein.
GN Names=rpsml; Synonyms=RPMS1;
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C15;
RX MEDLINE=20173697; PubMed=10708423;
RX DOI=10.1128/JVI.74.7.3082-3092.2000;
RA Smith P.R., de Jesus O.D., Turner D., Hollyoake M.,
RA Elgueta Karstegi C., Griffin B.E., Karran L., Wang Y., Hayward D.,
RA Farrell P.J.;
RT "Structure and coding content of CST (BART) family RNAs of Epstein-
RT Barr virus.";
RL J. Virol. 74:3082-3092(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=88283646; PubMed=2840285;
RA Laux G., Perricaudet M., Farrell P.J.;
RT "A spliced Epstein-Barr virus gene expressed in immortalized
RT lymphocytes is created by circularization of the linear viral

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Db          37 GQPR 40
RESULT 67
VPR_HV2ST
ID_VPR_HV2ST STANDARD; PRT; 104 AA.
AC P20884;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 2 (isolate ST) (HIV-2).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11721;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90112662; PubMed=2296086;
RA Kumar P., Hui H., Kappes J.C., Haggarty B.S., Hoxie J.A., Arya S.K.,
RA Shaw G.M., Hahn B.H.;
RT "Molecular characterization of an attenuated human immunodeficiency
RT virus type 2 isolate.";
RL J. Virol. 64:890-901(1990).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; J04498; AAB00749.1; -
DR HSSP; P12520; LDSK
DR HIV; J04498; VPR$21SY.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
SQ SEQUENCE 105 AA; 11975 MW; 3E17584B2DOCC64F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 87 GQPR 90

RESULT 69
O9FTT2 PRELIMINARY; PRT; 106 AA.
ID O9FTT2 AC O9FTT2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OSJNBa0086P08.25 protein (OSJNBa0010K01.6 protein).
GN Name=OSJNBa0086P08.25; Synonyms=OSJNBa0010K01.6;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takasaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojohori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF002855; BAB17214.1; -
DR EMBL; AF003210; BAB40093.1; -
DR Gramene; Q9FTT2; -
SQ SEQUENCE 106 AA; 12148 MW; A677EE54D485E8EC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 78 GQPR 81

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RESULT 70
Q98159 ID Q98159 PRELIMINARY; PRT; 106 AA.
AC Q98159;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein At2g16590.
GN Name=Atg16590;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Town C.D., Kaul S.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007195; AAD26488.1; -.
DR PIR; G84541; G84541.
KW Hypothetical protein.
SQ SEQUENCE 106 AA; 12519 MW; 00851E4AA6DB4363 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 55 GQPR 58

RESULT 71
Q92NZ1 ID Q92NZ1 PRELIMINARY; PRT; 106 AA.
AC Q92NZ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSMEMBRANE PROTEIN.
ORFNames=SMC04181;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubier F., Couzy J., Boche G., Ampe F., Batut J.,
RA Boisdard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godard T., Goffeau A., Kahn D., Kles E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46589.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 106 AA; 12105 MW; AEBOEAF31CDB67F4 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 72
Q7R3Y4 ID Q7R3Y4 PRELIMINARY; PRT; 107 AA.
AC Q7R3Y4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 68 62183 61860.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000012; EAA42044.1; -.
SQ SEQUENCE 107 AA; 11695 MW; CFC5D58B8B27648 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 97 GQPR 100

RESULT 73
Q820P4 ID Q820P4 PRELIMINARY; PRT; 108 AA.
AC Q820P4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome c, class IC: Cytochrome c, class I.
GN OrderedLocusNames=NE0736;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX323858; CAD84647.1; -.
DR HSSP; P82903; ICNO.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR009056; Cytochrome_c.
DR InterPro; IPR003088; Cyt_C1.
DR InterPro; IPR008189; Cyt_C_bact.
DR Pfam; PF00034; Cytochrom C; 1.
DR ProDom; PD004020; Cyt C_bact; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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KW Complete proteome.
SQ SEQUENCE 108 AA; 11550 MW; DE2337BCAA0FD793 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 56 GQPR 59

RESULT 74

Q9YDJ3 PRELIMINARY; PRT; 109 AA.
AC Q9YDJ3;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein APE0920.
GN OrderedLocusNames=APE0920;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000060; BAA79904.1; --
DR PIR; H72687;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 109 AA; 12293 MW; E9BDC6919B254CF1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 24 GQPR 27

RESULT 75

Q8S5J0 PRELIMINARY; PRT; 109 AA.
AC Q8S5J0;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein OSJNBa0011A24.25.
GN Names=OSJNBa0011A24.25;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
RA Kuit K., Nascimben L., Zuber V., Balija V., Bell M., Baker J.,
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC113336; AAM01182.2; --
DR Gramene; Q8S5J0; --
KW Hypothetical protein.
SQ SEQUENCE 109 AA; 11946 MW; 4632E8398432CFE2 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GQPR 4
Db 36 GQPR 39

Search completed: May 17, 2005, 10:08:23
Job time : 98 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 10:00:57 ; Search time 23 Seconds
(without alignments)
12.982 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata1/iaa/5A_COMB.pep.*

2: /cgn2_6/prodata1/iaa/5B_COMB.pep.*

3: /cgn2_6/prodata1/iaa/6A_COMB.pep.*

4: /cgn2_6/prodata1/iaa/6B_COMB.pep.*

5: /cgn2_6/prodata1/iaa/PCUS_COMB.pep.*

6: /cgn2_6/prodata1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	23	100.0	9	4	US-09-988-113-8
4	23	100.0	10	3	US-09-181-336-1
5	23	100.0	10	3	US-09-252-586-21
6	23	100.0	14	3	US-09-261-855-3
7	23	100.0	14	4	US-09-873-637-3
8	23	100.0	18	1	US-08-471-780C-109
9	23	100.0	18	1	US-08-471-780C-110
10	23	100.0	18	1	US-08-471-780C-111
11	23	100.0	18	1	US-08-467-282B-109
12	23	100.0	18	1	US-08-467-282B-110
13	23	100.0	18	1	US-08-467-282B-111
14	23	100.0	18	2	US-08-471-282A-109
15	23	100.0	18	2	US-08-471-282A-110
16	23	100.0	18	2	US-08-471-282A-111
17	23	100.0	18	2	US-08-466-710C-109
18	23	100.0	18	2	US-08-466-710C-110
19	23	100.0	18	2	US-08-466-710C-111
20	23	100.0	18	3	US-08-468-739C-109
21	23	100.0	18	3	US-08-468-739C-110
22	23	100.0	18	3	US-08-468-739C-111
23	23	100.0	18	4	US-09-293-769A-109
24	23	100.0	18	4	US-09-293-769A-110
25	23	100.0	18	4	US-09-293-769A-111
26	23	100.0	19	1	US-08-471-780C-115
27	23	100.0	19	1	US-08-471-780C-116

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29	23	100.0	19	1	US-08-467-282B-115	Sequence 115, App
30	23	100.0	19	1	US-08-467-282B-116	Sequence 116, App
31	23	100.0	19	1	US-08-467-282B-117	Sequence 117, App
32	23	100.0	19	2	US-08-471-282A-115	Sequence 115, App
33	23	100.0	19	2	US-08-471-282A-116	Sequence 116, App
34	23	100.0	19	2	US-08-471-282A-117	Sequence 117, App
35	23	100.0	19	2	US-08-466-710C-115	Sequence 115, App
36	23	100.0	19	2	US-08-466-710C-116	Sequence 116, App
37	23	100.0	19	2	US-08-466-710C-117	Sequence 117, App
38	23	100.0	19	3	US-08-468-739C-115	Sequence 115, App
39	23	100.0	19	3	US-08-468-739C-116	Sequence 116, App
40	23	100.0	19	3	US-08-468-739C-117	Sequence 117, App
41	23	100.0	19	4	US-09-293-769A-115	Sequence 115, App
42	23	100.0	19	4	US-09-293-769A-116	Sequence 116, App
43	23	100.0	19	4	US-09-293-769A-117	Sequence 117, App
44	23	100.0	20	3	US-08-851-843A-194	Sequence 194, App
45	23	100.0	20	3	US-08-974-549A-313	Sequence 313, App
46	23	100.0	20	3	US-08-854-050-194	Sequence 194, App
47	23	100.0	20	3	US-09-430-323-194	Sequence 194, App
48	23	100.0	20	4	US-09-402-181B-313	Sequence 313, App
49	23	100.0	20	4	US-09-721-456-313	Sequence 313, App
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51	23	100.0	28	3	US-09-088-154-1	Sequence 1, Appli
52	23	100.0	31	2	US-08-809-440-16	Sequence 16, Appli
53	23	100.0	33	4	US-09-523-686-2	Sequence 2, Appli
54	23	100.0	35	4	US-10-038-612-70	Sequence 70, Appli
55	23	100.0	37	4	US-09-461-325-262	Sequence 262, App
56	23	100.0	37	4	US-10-012-542-262	Sequence 262, App
57	23	100.0	37	4	US-10-115-123-262	Sequence 262, App
58	23	100.0	38	2	US-08-809-440-15	Sequence 15, Appli
59	23	100.0	41	1	US-08-548-540-94	Sequence 94, Appli
60	23	100.0	41	5	PC-T-US96-09809-94	Sequence 94, Appli
61	23	100.0	43	2	US-08-488-161-66	Sequence 66, Appli
62	23	100.0	43	3	US-09-273-685-66	Sequence 66, Appli
63	23	100.0	43	5	PC-T-US95-11934-66	Sequence 66, Appli
64	23	100.0	45	1	US-08-548-540-93	Sequence 93, Appli
65	23	100.0	45	5	PC-T-US96-09809-93	Sequence 93, Appli
66	23	100.0	47	2	US-08-809-440-17	Sequence 17, Appli
67	23	100.0	53	4	US-09-434-840-65	Sequence 65, Appli
68	23	100.0	55	4	US-09-270-767-42207	Sequence 42207, A
69	23	100.0	58	4	US-09-270-767-60731	Sequence 60731, A
70	23	100.0	60	4	US-09-489-039A-8043	Sequence 8043, Ap
71	23	100.0	60	4	US-09-248-796A-27059	Sequence 27059, A
72	23	100.0	68	4	US-08-754-477A-139	Sequence 139, App
73	23	100.0	74	3	US-09-227-357-163	Sequence 163, App
74	23	100.0	74	4	US-09-270-767-32321	Sequence 32321, A
75	23	100.0	74	4	US-09-270-767-47538	Sequence 47538, A
76	23	100.0	77	4	US-09-621-976-7616	Sequence 7616, Ap
77	23	100.0	81	4	US-09-621-976-5235	Sequence 5255, Ap
78	23	100.0	85	2	US-08-479-078-12	Sequence 12, Appli
79	23	100.0	85	4	US-09-621-976-4773	Sequence 4773, Ap
80	23	100.0	89	4	US-09-621-976-4646	Sequence 4646, App
81	23	100.0	90	4	US-09-673-395A-518	Sequence 518, App
82	23	100.0	92	4	US-09-270-767-37931	Sequence 37931, A
83	23	100.0	92	4	US-09-270-767-53148	Sequence 53148, A
84	23	100.0	95	4	US-09-252-991A-16640	Sequence 16640, A
85	23	100.0	106	3	US-08-505-533-5	Sequence 5, Appli
86	23	100.0	107	1	US-08-399-106A-9	Sequence 9, Appli
87	23	100.0	107	1	US-08-399-106A-10	Sequence 10, Appli
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93	23	100.0	107	2	US-08-434-869A-10	Sequence 10, Appli
94	23	100.0	107	2	US-08-434-869A-11	Sequence 11, Appli
95	23	100.0	107	2	US-08-070-116A-5	Sequence 5, Appli
96	23	100.0	107	3	US-08-444-644-22	Sequence 22, Appli
97	23	100.0	107	3	US-08-444-644-39	Sequence 39, Appli
98	23	100.0	107	3	US-08-444-644-45	Sequence 45, Appli
99	23	100.0	107	3	US-09-102-528-23	Sequence 23, Appli
100	23	100.0	107	3	US-09-102-528-27	Sequence 27, Appli

101	23	100.0	107	3	US-08-232-246A-22	Sequence 22, Appl	174	23	100.0	169	4	US-09-252-991A-26569	Sequence 26569, A
102	23	100.0	107	3	US-08-232-246A-39	Sequence 39, Appl	175	23	100.0	169	4	US-09-252-991A-31908	Sequence 31908, A
103	23	100.0	107	3	US-08-232-246A-45	Sequence 45, Appl	176	23	100.0	170	4	US-09-252-991A-21669	Sequence 21669, A
104	23	100.0	107	4	US-08-557-050-5	Sequence 5, Appl	177	23	100.0	170	4	US-09-252-991A-23814	Sequence 23814, A
105	23	100.0	108	1	US-08-399-106A-1	Sequence 1, Appl	178	23	100.0	170	4	US-09-489-039A-7335	Sequence 7335, Ap
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107	23	100.0	108	1	US-08-399-106A-3	Sequence 3, Appl	180	23	100.0	178	4	US-09-252-991A-28980	Sequence 28980, A
108	23	100.0	108	1	US-08-399-106A-8	Sequence 8, Appl	181	23	100.0	179	4	US-09-252-991A-28872	Sequence 28872, A
109	23	100.0	108	1	US-08-433-105A-1	Sequence 1, Appl	182	23	100.0	180	4	US-09-231-788-2	Sequence 2, Appl
110	23	100.0	108	1	US-08-433-105A-2	Sequence 2, Appl	183	23	100.0	180	4	US-09-620-958-2	Sequence 2, Appl
111	23	100.0	108	1	US-08-433-105A-3	Sequence 3, Appl	184	23	100.0	180	4	US-09-611-152-2	Sequence 2, Appl
112	23	100.0	108	1	US-08-433-105A-8	Sequence 8, Appl	185	23	100.0	180	4	US-09-252-991A-22780	Sequence 22780, A
113	23	100.0	108	1	US-08-434-869A-1	Sequence 1, Appl	186	23	100.0	180	4	US-09-480-297A-2	Sequence 2, Appl
114	23	100.0	108	2	US-08-434-869A-2	Sequence 2, Appl	187	23	100.0	180	4	US-09-794-705A-2	Sequence 2, Appl
115	23	100.0	108	2	US-08-434-869A-3	Sequence 3, Appl	188	23	100.0	180	4	US-09-747-259-2	Sequence 2, Appl
116	23	100.0	108	2	US-08-434-869A-8	Sequence 8, Appl	189	23	100.0	180	4	US-09-816-744-2	Sequence 2, Appl
117	23	100.0	110	4	US-09-270-767-41219	Sequence 41219, A	190	23	100.0	180	4	US-09-631-531-2	Sequence 2, Appl
118	23	100.0	110	4	US-09-270-767-56435	Sequence 56435, A	191	23	100.0	181	4	US-09-252-991A-23717	Sequence 23717, A
119	23	100.0	112	4	US-09-640-211A-1119	Sequence 1119, Ap	192	23	100.0	183	4	US-09-252-991A-26451	Sequence 26451, A
120	23	100.0	113	3	US-09-284-033-7	Sequence '7, Appl	193	23	100.0	184	4	US-09-902-540-10529	Sequence 10529, A
121	23	100.0	113	3	US-08-729-834B-7	Sequence 7, Appl	194	23	100.0	185	4	US-09-252-991A-23309	Sequence 23309, A
122	23	100.0	113	4	US-09-489-039A-10098	Sequence 10098, A	195	23	100.0	188	4	US-09-252-991A-26775	Sequence 26775, A
123	23	100.0	116	4	US-09-902-540-14679	Sequence 14679, A	196	23	100.0	193	2	US-08-469-537A-34	Sequence 34, Appl
124	23	100.0	123	3	US-09-102-528-22	Sequence 22, Appl	197	23	100.0	193	4	US-09-252-991A-25174	Sequence 25174, A
125	23	100.0	123	3	US-09-102-528-22	Sequence 22, Appl	198	23	100.0	193	4	US-09-949-016-10191	Sequence 10191, A
126	23	100.0	124	4	US-09-673-395A-608	Sequence 608, App	199	23	100.0	194	4	US-09-489-039A-11206	Sequence 11206, A
127	23	100.0	124	4	US-09-543-681A-6502	Sequence 6502, Ap	200	23	100.0	194	4	US-09-134-000C-6476	Sequence 6476, Ap
128	23	100.0	125	4	US-09-902-540-16622	Sequence 16622, A	201	23	100.0	199	4	US-09-252-991A-27431	Sequence 27431, A
129	23	100.0	126	4	US-09-231-788-15	Sequence 15, Appl	202	23	100.0	200	4	US-09-252-991A-20400	Sequence 20400, A
130	23	100.0	128	3	US-09-227-357-190	Sequence 190, App	203	23	100.0	201	3	US-09-220-528-116	Sequence 116, App
131	23	100.0	129	4	US-09-270-767-41353	Sequence 41353, A	204	23	100.0	201	4	US-09-252-991A-21893	Sequence 21893, A
132	23	100.0	129	4	US-09-270-767-56569	Sequence 56569, A	205	23	100.0	201	4	US-09-252-991A-24176	Sequence 24176, A
133	23	100.0	133	4	US-09-489-039A-13192	Sequence 13192, A	206	23	100.0	201	4	US-09-252-991A-27995	Sequence 27995, A
134	23	100.0	134	4	US-08-469-260A-189	Sequence 189, App	207	23	100.0	202	4	US-09-461-325-261	Sequence 261, App
135	23	100.0	134	4	US-09-252-991A-23970	Sequence 23970, A	208	23	100.0	202	4	US-09-489-039A-8112	Sequence 8112, App
136	23	100.0	134	4	US-09-252-991A-26959	Sequence 26959, A	209	23	100.0	202	4	US-10-012-542-261	Sequence 261, App
137	23	100.0	134	4	US-09-252-991A-31289	Sequence 31289, A	210	23	100.0	202	4	US-09-270-767-34039	Sequence 34039, A
138	23	100.0	134	4	US-08-488-446-189	Sequence 189, App	211	23	100.0	202	4	US-09-270-767-49256	Sequence 49256, A
139	23	100.0	134	4	US-08-467-344A-189	Sequence 189, App	212	23	100.0	202	4	US-09-248-796A-27997	Sequence 27997, A
140	23	100.0	134	4	US-08-424-550B-189	Sequence 189, App	213	23	100.0	202	4	US-10-115-123-261	Sequence 261, App
141	23	100.0	135	4	US-09-270-767-39535	Sequence 39535, A	214	23	100.0	204	4	US-09-489-039A-7643	Sequence 7643, Ap
142	23	100.0	135	4	US-09-270-767-54752	Sequence 54752, A	215	23	100.0	206	4	US-09-270-767-57339	Sequence 57339, A
143	23	100.0	137	4	US-09-270-767-32755	Sequence 32755, A	216	23	100.0	209	4	US-09-248-796A-24290	Sequence 24290, A
144	23	100.0	137	4	US-09-270-767-47972	Sequence 47972, A	217	23	100.0	211	4	US-09-252-991A-36573	Sequence 26573, A
145	23	100.0	137	4	US-09-248-796A-18077	Sequence 18077, A	218	23	100.0	212	1	US-08-430-633-4	Sequence 4, Appl
146	23	100.0	141	4	US-09-252-991A-19268	Sequence 19268, A	219	23	100.0	212	2	US-08-620-694A-4	Sequence 4, Appl
147	23	100.0	143	4	US-09-252-991A-32704	Sequence 32704, A	220	23	100.0	212	2	US-08-936-854-4	Sequence 4, Appl
148	23	100.0	147	4	US-09-270-767-46762	Sequence 46762, A	221	23	100.0	212	3	US-09-022-255-4	Sequence 4, Appl
149	23	100.0	148	4	US-09-252-991A-21248	Sequence 21248, A	222	23	100.0	212	3	US-09-022-696-4	Sequence 4, Appl
150	23	100.0	148	4	US-09-434-840-30	Sequence 30, Appl	223	23	100.0	212	3	US-09-022-253-4	Sequence 4, Appl
151	23	100.0	149	4	US-09-252-991A-32070	Sequence 32070, A	224	23	100.0	212	3	US-09-022-260-4	Sequence 4, Appl
152	23	100.0	153	4	US-09-252-991A-27025	Sequence 27025, A	225	23	100.0	212	3	US-09-022-259-4	Sequence 4, Appl
153	23	100.0	153	4	US-09-270-767-45238	Sequence 45238, A	226	23	100.0	212	3	US-09-022-257-4	Sequence 4, Appl
154	23	100.0	153	4	US-09-902-540-11548	Sequence 11548, A	227	23	100.0	212	4	US-09-252-991A-19448	Sequence 19448, A
155	23	100.0	154	4	US-09-252-991A-26832	Sequence 26832, A	228	23	100.0	212	4	US-09-549-679-4	Sequence 4, Appl
156	23	100.0	154	4	US-09-252-991A-31305	Sequence 31305, A	229	23	100.0	212	4	US-10-033-522-2	Sequence 2, Appl
157	23	100.0	155	4	US-09-975-456B-10	Sequence 10, Appl	230	23	100.0	213	4	US-09-252-991A-29496	Sequence 29496, A
158	23	100.0	156	4	US-09-252-991A-31384	Sequence 31384, A	231	23	100.0	213	4	US-09-328-352-6121	Sequence 6121, Ap
159	23	100.0	156	4	US-09-621-976-4844	Sequence 4844, Ap	232	23	100.0	214	4	US-09-248-796A-21566	Sequence 21566, A
160	23	100.0	159	4	US-09-252-991A-19997	Sequence 19997, A	233	23	100.0	216	4	US-09-248-796A-18824	Sequence 18824, A
161	23	100.0	160	4	US-09-270-767-31703	Sequence 31703, A	234	23	100.0	217	4	US-09-483-588-5	Sequence 5, Appl
162	23	100.0	161	4	US-09-270-767-35934	Sequence 35934, A	235	23	100.0	218	4	US-09-483-588-3	Sequence 3, Appl
163	23	100.0	161	4	US-09-270-767-51151	Sequence 51151, A	236	23	100.0	218	4	US-09-483-588-4	Sequence 4, Appl
164	23	100.0	162	4	US-09-640-211A-1104	Sequence 1104, Ap	237	23	100.0	218	4	US-09-483-588-6	Sequence 6, Appl
165	23	100.0	163	3	US-09-199-637A-335	Sequence 335, App	238	23	100.0	218	4	US-09-483-588-7	Sequence 7, Appl
166	23	100.0	163	3	US-08-966-317-1	Sequence 1, Appl	239	23	100.0	219	4	US-09-252-991A-17169	Sequence 17169, A
167	23	100.0	165	3	US-09-489-770-1	Sequence 1, Appl	240	23	100.0	223	4	US-09-252-991A-17855	Sequence 17855, A
168	23	100.0	165	4	US-09-902-540-13688	Sequence 13688, A	241	23	100.0	224	4	US-09-710-279-496	Sequence 496, App
169	23	100.0	166	4	US-09-252-991A-20239	Sequence 20239, A	242	23	100.0	224	4	US-09-710-279-1366	Sequence 1366, Ap
170	23	100.0	169	4	US-09-252-991A-20992	Sequence 20992, A	243	23	100.0	225	4	US-09-252-991A-27348	Sequence 27348, A
171	23	100.0	169	4	US-09-252-991A-22999	Sequence 22999, A	244	23	100.0	227	3	US-08-911-853-23	Sequence 23, Appl
172	23	100.0	169	4	US-09-252-991A-24746	Sequence 24746, A	245	23	100.0	227	3	US-09-479-409-23	Sequence 23, Appl
173	23	100.0	169	4	US-09-252-991A-25204	Sequence 25204, A	246	23	100.0	227	3	US-09-479-453-23	Sequence 23, Appl

247	23	100.0	227	4	US-09-461-325-211	Sequence 211, App	320	23	100.0	245	4	US-08-424-550B-40	Sequence 40, Appl
248	23	100.0	227	4	US-10-012-542-211	Sequence 211, App	321	23	100.0	246	4	US-09-252-991A-31095	Sequence 31095, A
249	23	100.0	227	4	US-10-115-123-211	Sequence 211, App	322	23	100.0	247	4	US-09-428-082B-6	Sequence 6, Appli
250	23	100.0	228	3	US-09-134-001C-5384	Sequence 5384, Ap	323	23	100.0	247	4	US-09-428-082B-12	Sequence 12, Appl
251	23	100.0	228	4	US-09-489-039A-10548	Sequence 10548, A	324	23	100.0	248	4	US-09-252-991A-19942	Sequence 19942, A
252	23	100.0	228	4	US-09-428-082B-2	Sequence 2, Appli	325	23	100.0	248	4	US-09-252-991A-21872	Sequence 21872, A
253	23	100.0	228	4	US-09-847-249A-2	Sequence 2, Appli	326	23	100.0	248	4	US-09-252-991A-30679	Sequence 30679, A
254	23	100.0	228	4	US-09-840-669B-2	Sequence 2, Appli	327	23	100.0	248	4	US-09-428-082B-10567	Sequence 1056, Ap
255	23	100.0	228	4	US-09-843-221A-2	Sequence 2, Appli	328	23	100.0	248	4	US-09-428-082B-1058	Sequence 1058, Ap
256	23	100.0	228	4	US-09-968-362A-27	Sequence 27, Appl	329	23	100.0	248	4	US-09-428-082B-1068	Sequence 1060, Ap
257	23	100.0	228	4	US-09-709-704B-2	Sequence 2, Appli	330	23	100.0	248	4	US-09-428-082B-1062	Sequence 1062, Ap
258	23	100.0	228	4	US-09-422-838C-5	Sequence 5, Appli	331	23	100.0	250	4	US-09-428-082B-1070	Sequence 1070, Ap
259	23	100.0	229	4	US-09-122-144-2	Sequence 2, Appli	332	23	100.0	250	4	US-09-248-796A-27542	Sequence 27542, A
260	23	100.0	229	4	US-09-252-991A-19104	Sequence 19104, A	333	23	100.0	252	4	US-09-428-082B-1064	Sequence 1064, Ap
261	23	100.0	229	4	US-09-252-991A-27802	Sequence 27802, A	334	23	100.0	252	4	US-09-428-082B-1066	Sequence 1066, Ap
262	23	100.0	229	4	US-09-252-991A-27907	Sequence 27907, A	335	23	100.0	252	4	US-09-976-594-112	Sequence 112, App
263	23	100.0	229	4	US-09-968-362A-28	Sequence 28, Appl	336	23	100.0	253	4	US-09-252-991A-28659	Sequence 28659, A
264	23	100.0	230	4	US-09-252-991A-16763	Sequence 16763, A	337	23	100.0	253	4	US-09-428-082B-16	Sequence 16, Appl
265	23	100.0	230	4	US-09-252-991A-28838	Sequence 28838, A	338	23	100.0	253	4	US-09-428-082B-18	Sequence 18, Appl
266	23	100.0	231	4	US-09-252-991A-22663	Sequence 22663, A	339	23	100.0	254	4	US-08-284-391B-33	Sequence 33, Appl
267	23	100.0	231	4	US-09-252-991A-22962	Sequence 22962, A	340	23	100.0	254	3	US-09-218-950-33	Sequence 33, Appl
268	23	100.0	231	4	US-09-248-796A-27586	Sequence 27586, A	341	23	100.0	254	4	US-09-252-991A-25445	Sequence 25445, A
269	23	100.0	232	1	US-07-797-556-4	Sequence 4, Appli	342	23	100.0	254	4	US-09-252-991A-32919	Sequence 32919, A
270	23	100.0	232	1	US-08-225-989-4	Sequence 4, Appli	343	23	100.0	254	4	US-08-394-388A-33	Sequence 33, Appl
271	23	100.0	232	1	US-08-570-923-4	Sequence 4, Appli	344	23	100.0	256	4	US-09-252-991A-29557	Sequence 29557, A
272	23	100.0	232	1	US-08-580-014-4	Sequence 4, Appli	345	23	100.0	256	4	US-09-902-540-11957	Sequence 11957, A
273	23	100.0	232	1	US-08-308-881-4	Sequence 4, Appli	346	23	100.0	256	4	US-09-252-991A-25689	Sequence 25689, A
274	23	100.0	232	2	US-09-058-263-4	Sequence 4, Appli	347	23	100.0	259	4	US-09-808-701A-18	Sequence 18, Appl
275	23	100.0	232	2	US-09-059-099-4	Sequence 4, Appli	348	23	100.0	260	4	US-09-071-252-12	Sequence 12, Appl
276	23	100.0	232	2	US-08-595-043A-50	Sequence 50, Appl	349	23	100.0	261	4	US-09-252-991A-16803	Sequence 16803, A
277	23	100.0	232	3	US-09-058-264-4	Sequence 4, Appli	350	23	100.0	261	4	US-09-252-991A-23563	Sequence 23563, A
278	23	100.0	232	3	US-08-996-139-8	Sequence 8, Appli	351	23	100.0	261	4	US-09-071-252-10	Sequence 10, Appl
279	23	100.0	232	3	US-09-079-785-4	Sequence 4, Appli	352	23	100.0	262	4	US-09-902-540-11432	Sequence 11432, A
280	23	100.0	232	3	US-08-995-659-8	Sequence 8, Appli	353	23	100.0	263	4	US-09-818-780-32	Sequence 32, Appl
281	23	100.0	232	3	US-09-215-649A-8	Sequence 8, Appli	354	23	100.0	263	4	US-09-818-780-88	Sequence 88, Appl
282	23	100.0	232	4	US-09-577-800-8	Sequence 8, Appli	355	23	100.0	263	4	US-09-270-767-32374	Sequence 32374, A
283	23	100.0	232	4	US-09-577-800-8	Sequence 8, Appli	356	23	100.0	263	4	US-09-270-767-47591	Sequence 47591, A
284	23	100.0	232	4	US-09-455-962-4	Sequence 4, Appli	357	23	100.0	264	4	US-09-252-991A-30092	Sequence 30092, A
285	23	100.0	232	4	US-09-466-496-8	Sequence 4, Appli	358	23	100.0	265	4	US-09-252-991A-29150	Sequence 29150, A
286	23	100.0	232	4	US-09-871-856-8	Sequence 8, Appli	359	23	100.0	268	4	US-09-428-082B-8	Sequence 8, Appli
287	23	100.0	232	4	US-09-252-991A-17146	Sequence 17146, A	360	23	100.0	269	2	US-08-727-311-3	Sequence 3, Appli
288	23	100.0	232	4	US-09-871-291-8	Sequence 8, Appli	361	23	100.0	269	3	US-09-111-556A-4	Sequence 4, Appli
289	23	100.0	232	4	US-09-877-650-8	Sequence 8, Appli	362	23	100.0	269	3	US-08-360-758-4	Sequence 4, Appli
290	23	100.0	232	4	US-09-628-126-4	Sequence 4, Appli	363	23	100.0	269	4	US-09-252-991A-20973	Sequence 20973, A
291	23	100.0	232	4	US-09-865-363-8	Sequence 8, Appli	364	23	100.0	269	4	US-09-428-082B-10	Sequence 10, Appl
292	23	100.0	232	4	US-09-968-362A-26	Sequence 26, Appl	365	23	100.0	269	4	US-09-422-838C-46	Sequence 46, Appl
293	23	100.0	232	4	PCT-US95-06530-4	Sequence 8, Appli	366	23	100.0	270	4	US-09-252-991A-18185	Sequence 18185, A
294	23	100.0	232	5	PCT-US95-15781-8	Sequence 4, Appli	367	23	100.0	270	4	US-09-540-236-3122	Sequence 3122, Ap
295	23	100.0	232	4	US-08-756-416-33	Sequence 8, Appli	368	23	100.0	271	4	US-09-252-991A-23010	Sequence 23010, A
296	23	100.0	234	4	US-08-591-989-2	Sequence 33, Appl	369	23	100.0	272	4	US-09-252-991A-31806	Sequence 31806, A
297	23	100.0	235	3	US-09-131-247-6	Sequence 6, Appli	370	23	100.0	273	4	US-09-252-991A-16693	Sequence 16693, A
298	23	100.0	235	4	US-09-784-623-6	Sequence 6, Appli	371	23	100.0	273	4	US-09-252-991A-17447	Sequence 17447, A
299	23	100.0	235	4	US-09-302-540-11606	Sequence 11606, A	372	23	100.0	273	4	US-09-252-991A-22485	Sequence 22485, A
300	23	100.0	235	4	US-09-134-000C-6559	Sequence 6559, Ap	373	23	100.0	273	4	US-09-252-991A-32405	Sequence 32405, A
301	23	100.0	238	4	US-09-252-991A-26949	Sequence 26949, A	374	23	100.0	275	4	US-09-252-991A-17995	Sequence 17995, A
302	23	100.0	239	4	US-09-252-991A-17237	Sequence 17237, A	375	23	100.0	276	4	US-09-252-991A-23623	Sequence 23623, A
303	23	100.0	240	4	US-09-252-991A-17237	Sequence 17237, A	376	23	100.0	277	4	US-09-428-082B-20	Sequence 20, Appl
304	23	100.0	240	4	US-09-252-991A-17701	Sequence 17701, A	377	23	100.0	277	4	US-09-428-082B-22	Sequence 22, Appl
305	23	100.0	240	4	US-09-252-991A-19090	Sequence 19090, A	378	23	100.0	279	4	US-09-252-991A-32443	Sequence 32443, A
306	23	100.0	240	4	US-09-270-767-57173	Sequence 57173, A	379	23	100.0	281	4	US-09-252-991A-17748	Sequence 17748, A
307	23	100.0	241	4	US-09-640-211A-819	Sequence 819, App	380	23	100.0	281	4	US-09-854-864-10	Sequence 10, Appl
308	23	100.0	242	4	US-09-252-991A-32268	Sequence 32268, A	381	23	100.0	282	4	US-09-252-991A-28598	Sequence 28598, A
309	23	100.0	243	4	US-09-428-082B-17307	Sequence 17307, A	382	23	100.0	282	4	US-09-949-016-8392	Sequence 8392, Ap
310	23	100.0	243	4	US-09-428-082B-1068	Sequence 1068, Ap	383	23	100.0	283	4	US-09-854-864-9	Sequence 9, Appli
311	23	100.0	243	4	US-09-302-540-13234	Sequence 13234, A	384	23	100.0	284	4	US-09-387-375-7	Sequence 7, Appli
312	23	100.0	245	1	US-07-943-843-8	Sequence 8, Appli	385	23	100.0	284	4	US-10-041-400A-7	Sequence 7, Appli
313	23	100.0	245	1	US-08-236-918A-15	Sequence 15, Appl	386	23	100.0	284	4	US-10-042-991A-7	Sequence 7, Appli
314	23	100.0	245	1	US-08-347-003-8	Sequence 8, Appli	387	23	100.0	286	4	US-09-252-991A-24111	Sequence 24111, A
315	23	100.0	245	3	US-09-150-864A-15	Sequence 15, Appl	388	23	100.0	286	4	US-09-252-991A-30343	Sequence 30343, A
316	23	100.0	245	4	US-08-469-260A-40	Sequence 40, Appl	389	23	100.0	287	4	US-09-252-991A-19944	Sequence 19944, A
317	23	100.0	245	4	US-08-488-446-40	Sequence 40, Appl	390	23	100.0	289	4	US-09-252-991A-17482	Sequence 17482, A
318	23	100.0	245	4	US-08-467-344A-40	Sequence 40, Appl	391	23	100.0	289	4	US-09-252-991A-23728	Sequence 23728, A
319	23	100.0	245	4	US-09-489-039A-14192	Sequence 14192, A	392	23	100.0	290	4	US-08-484-841A-8	Sequence 8, Appli

539	23	100.0	375	4	US-09-902-540-15899	Sequence 15899, A	612	23	100.0	420	4	US-09-252-991A-19117	Sequence 19117, A
540	23	100.0	376	3	US-09-180-100-22	Sequence 22, Appl	613	23	100.0	420	4	US-09-252-991A-25649	Sequence 25649, A
541	23	100.0	376	4	US-09-252-991A-21843	Sequence 21843, A	614	23	100.0	423	4	US-09-252-991A-18694	Sequence 18694, A
542	23	100.0	377	2	US-08-761-277A-45	Sequence 45, Appl	615	23	100.0	423	4	US-09-252-991A-29867	Sequence 29867, A
543	23	100.0	377	4	US-09-227-595-24	Sequence 24, Appl	616	23	100.0	423	4	US-09-832-659A-44	Sequence 44, Appl
544	23	100.0	377	4	US-08-595-390B-24	Sequence 24, Appl	617	23	100.0	424	3	US-09-333-593A-8	Sequence 8, Appl
545	23	100.0	377	4	US-09-949-016-10067	Sequence 10067, A	618	23	100.0	424	5	PCT-US95-03866-12	Sequence 12, Appl
546	23	100.0	377	4	US-09-949-016-10068	Sequence 10068, A	619	23	100.0	424	5	PCT-US95-03866-14	Sequence 14, Appl
547	23	100.0	380	3	US-09-181-336-17	Sequence 17, Appl	620	23	100.0	425	4	US-09-252-991A-17186	Sequence 17186, A
548	23	100.0	380	3	US-09-181-336-19	Sequence 19, Appl	621	23	100.0	428	4	US-09-902-540-13785	Sequence 13785, A
549	23	100.0	381	4	US-09-252-991A-28320	Sequence 28320, A	622	23	100.0	429	2	US-09-074-512-1	Sequence 1, Appl
550	23	100.0	382	1	US-08-470-299-7	Sequence 7, Appl	623	23	100.0	429	4	US-09-372-425A-6	Sequence 6, Appl
551	23	100.0	382	1	US-08-470-299-10	Sequence 10, Appl	624	23	100.0	429	4	US-09-489-039A-10891	Sequence 10891, A
552	23	100.0	382	4	US-09-252-991A-29100	Sequence 29100, A	625	23	100.0	430	4	US-09-252-991A-16681	Sequence 16681, A
553	23	100.0	385	4	US-09-252-991A-26432	Sequence 26432, A	626	23	100.0	430	4	US-09-252-991A-18400	Sequence 18400, A
554	23	100.0	387	1	US-08-470-299-4	Sequence 4, Appl	627	23	100.0	430	4	US-09-252-991A-18437	Sequence 18437, A
555	23	100.0	388	3	US-09-131-247-16	Sequence 16, Appl	628	23	100.0	431	4	US-09-252-991A-28694	Sequence 28694, A
556	23	100.0	388	4	US-09-252-991A-21781	Sequence 21781, A	629	23	100.0	431	4	US-09-773-877B-27	Sequence 27, Appl
557	23	100.0	388	4	US-09-252-991A-21876	Sequence 21876, A	630	23	100.0	432	3	US-08-477-460B-2	Sequence 2, Appl
558	23	100.0	388	4	US-09-252-991A-24693	Sequence 24693, A	631	23	100.0	432	3	US-08-379-516-2	Sequence 2, Appl
559	23	100.0	388	4	US-09-784-623-16	Sequence 16, Appl	632	23	100.0	432	3	US-09-329-916-2	Sequence 2, Appl
560	23	100.0	389	3	US-09-131-247-14	Sequence 14, Appl	633	23	100.0	432	3	US-08-485-372A-2	Sequence 2, Appl
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562	23	100.0	389	4	US-09-784-623-14	Sequence 14, Appl	635	23	100.0	432	4	US-08-484-681-2	Sequence 2, Appl
563	23	100.0	390	4	US-09-252-991A-17829	Sequence 17829, A	636	23	100.0	432	4	US-09-252-991A-17067	Sequence 17067, A
564	23	100.0	392	4	US-09-252-991A-31291	Sequence 31291, A	637	23	100.0	432	4	US-09-252-991A-32301	Sequence 32301, A
565	23	100.0	393	1	US-08-689-974-4	Sequence 4, Appl	638	23	100.0	432	4	US-09-766-995-2	Sequence 2, Appl
566	23	100.0	393	3	US-09-058-376-4	Sequence 4, Appl	639	23	100.0	432	5	PCT-US93-07422-2	Sequence 2, Appl
567	23	100.0	393	4	US-09-252-991A-23307	Sequence 23307, A	640	23	100.0	433	4	US-09-252-991A-20044	Sequence 2, Appl
568	23	100.0	393	4	US-09-252-991A-24171	Sequence 24171, A	641	23	100.0	433	4	US-09-252-991A-32205	Sequence 32205, A
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572	23	100.0	396	4	US-09-252-991A-24697	Sequence 24697, A	645	23	100.0	434	4	US-08-472-888A-4	Sequence 4, Appl
573	23	100.0	397	4	US-08-775-066-2	Sequence 2, Appl	646	23	100.0	436	4	US-09-734-673-2	Sequence 2, Appl
574	23	100.0	397	4	US-09-854-864-18	Sequence 18, Appl	647	23	100.0	436	4	US-09-523-849-2	Sequence 2, Appl
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586	23	100.0	401	4	US-09-270-767-52851	Sequence 52851, A	659	23	100.0	442	1	US-08-461-968A-2	Sequence 2, Appl
587	23	100.0	401	4	US-09-248-796A-19514	Sequence 19514, A	660	23	100.0	442	1	US-08-461-968A-5	Sequence 5, Appl
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593	23	100.0	405	4	US-09-489-039A-7341	Sequence 7341, Ap	666	23	100.0	442	5	PCT-US96-10043-9	Sequence 9, Appl
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596	23	100.0	408	4	US-09-252-991A-27849	Sequence 27849, A	669	23	100.0	443	5	PCT-US96-13152-4	Sequence 4, Appl
597	23	100.0	408	4	US-09-489-039A-8307	Sequence 8307, Ap	670	23	100.0	444	4	US-09-252-991A-28809	Sequence 28809, A
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599	23	100.0	409	4	US-09-328-352-4570	Sequence 4570, Ap	672	23	100.0	445	3	US-08-341-560B-17	Sequence 17, Appl
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686	23	100.0	449	4	US-09-680-148-2	Sequence 2, Appli	759	453	4	US-09-802-097-8	Sequence 8, Appli
687	23	100.0	449	4	US-09-304-465A-2	Sequence 2, Appli	760	453	4	US-10-212-507-6	Sequence 6, Appli
688	23	100.0	449	4	US-09-500-253B-23	Sequence 23, Appli	761	454	2	US-07-934-373C-22	Sequence 22, Appli
689	23	100.0	449	4	US-09-368-362A-20	Sequence 20, Appli	762	454	3	US-08-437-642B-22	Sequence 22, Appli
690	23	100.0	450	2	US-08-788-800-12	Sequence 12, Appli	763	454	3	US-08-146-206C-22	Sequence 22, Appli
691	23	100.0	450	4	US-09-532-856-5	Sequence 5, Appli	764	454	4	US-09-252-991A-28780	Sequence 28780, A
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693	23	100.0	450	4	US-09-324-100C-5	Sequence 5, Appli	766	454	4	US-09-705-392A-22	Sequence 22, Appli
694	23	100.0	450	4	US-10-212-507-5	Sequence 5, Appli	767	454	4	US-09-705-398-22	Sequence 22, Appli
695	23	100.0	450	4	US-09-596-288-208	Sequence 208, App	768	454	5	PCF-US93-07832-22	Sequence 22, Appli
696	23	100.0	450	4	US-09-596-288-210	Sequence 210, App	769	455	4	US-09-773-877B-24	Sequence 24, Appli
697	23	100.0	450	4	US-09-596-288-212	Sequence 212, App	770	456	4	US-09-252-991A-17335	Sequence 17335, A
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699	23	100.0	450	4	US-09-596-288-216	Sequence 216, App	772	458	4	US-09-773-877B-26	Sequence 26, Appli
700	23	100.0	450	4	US-09-596-288-218	Sequence 218, App	773	459	1	US-08-157-101A-7	Sequence 7, Appli
701	23	100.0	450	4	US-09-596-288-220	Sequence 220, App	774	461	4	US-09-252-991A-24667	Sequence 24667, A
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703	23	100.0	450	4	US-09-596-288-224	Sequence 224, App	776	462	4	US-09-252-991A-31817	Sequence 31817, A
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705	23	100.0	450	4	US-09-596-288-228	Sequence 228, App	778	462	4	US-09-773-877B-18	Sequence 18, Appli
706	23	100.0	450	4	US-09-596-288-232	Sequence 232, App	779	463	4	US-09-472-087-1	Sequence 1, Appli
707	23	100.0	450	4	US-09-596-288-234	Sequence 234, App	780	463	4	US-09-472-087-4	Sequence 4, Appli
708	23	100.0	450	4	US-09-596-288-236	Sequence 236, App	781	463	4	US-09-472-087-64	Sequence 64, Appli
709	23	100.0	450	4	US-09-596-288-238	Sequence 238, App	782	463	4	US-09-472-087-64	Sequence 64, Appli
710	23	100.0	450	4	US-09-596-288-240	Sequence 240, App	783	463	4	US-09-472-087-68	Sequence 68, Appli
711	23	100.0	450	4	US-09-596-288-242	Sequence 242, App	784	464	4	US-09-252-991A-27367	Sequence 27367, A
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713	23	100.0	450	4	US-09-596-288-246	Sequence 246, App	786	464	4	US-09-472-087-66	Sequence 66, Appli
714	23	100.0	450	4	US-09-596-288-248	Sequence 248, App	787	465	4	US-09-252-991A-20576	Sequence 20576, A
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716	23	100.0	450	4	US-09-596-288-252	Sequence 252, App	789	467	1	US-09-704-744-81	Sequence 81, Appli
717	23	100.0	450	4	US-09-596-288-254	Sequence 254, App	790	467	3	US-09-049-672A-8	Sequence 8, Appli
718	23	100.0	450	4	US-09-596-288-256	Sequence 256, App	791	467	3	US-08-523-894-8	Sequence 8, Appli
719	23	100.0	451	2	US-08-887-352B-18	Sequence 18, Appli	792	467	3	US-08-523-894-10	Sequence 10, Appli
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721	23	100.0	451	2	US-08-887-352B-18	Sequence 18, Appli	794	467	4	US-08-030-175-41	Sequence 41, Appli
722	23	100.0	451	3	US-08-466-151-65	Sequence 65, Appli	795	467	4	US-08-030-175-42	Sequence 42, Appli
723	23	100.0	451	3	US-09-109-207C-14	Sequence 14, Appli	796	468	3	US-09-485-737B-67	Sequence 67, Appli
724	23	100.0	451	3	US-09-109-207C-16	Sequence 16, Appli	797	468	4	US-09-252-991A-27575	Sequence 27575, A
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727	23	100.0	451	3	US-09-054-255-2	Sequence 2, Appli	800	469	2	US-07-934-373C-23	Sequence 23, Appli
728	23	100.0	451	3	US-09-296-005-14	Sequence 14, Appli	801	469	2	US-08-437-642B-23	Sequence 23, Appli
729	23	100.0	451	3	US-09-296-005-16	Sequence 16, Appli	802	469	4	US-08-146-206C-23	Sequence 23, Appli
730	23	100.0	451	3	US-09-296-005-18	Sequence 18, Appli	803	469	4	US-09-705-686-23	Sequence 23, Appli
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732	23	100.0	451	4	US-09-466-635-3	Sequence 3, Appli	805	469	4	US-09-705-398-23	Sequence 23, Appli
733	23	100.0	451	4	US-09-282-846-2	Sequence 2, Appli	806	470	4	US-09-859-053-28	Sequence 28, Appli
734	23	100.0	451	4	US-09-680-145-2	Sequence 14, Appli	807	470	4	US-09-859-053-32	Sequence 32, Appli
735	23	100.0	451	4	US-09-320-171-14	Sequence 16, Appli	808	470	4	US-09-859-053-36	Sequence 36, Appli
736	23	100.0	451	4	US-09-320-171-16	Sequence 16, Appli	809	472	3	US-08-793-450-8	Sequence 8, Appli
737	23	100.0	451	4	US-09-320-171-18	Sequence 18, Appli	810	472	4	US-09-301-593-30	Sequence 30, Appli
738	23	100.0	451	4	US-09-472-087-70	Sequence 70, Appli	811	472	4	US-09-301-593-43	Sequence 43, Appli
739	23	100.0	451	4	US-09-716-028-14	Sequence 14, Appli	812	472	4	US-09-252-991A-17011	Sequence 17011, A
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743	23	100.0	451	4	US-10-113-996-14	Sequence 14, Appli	816	473	2	US-08-484-624A-16	Sequence 16, Appli
744	23	100.0	451	4	US-10-113-996-16	Sequence 16, Appli	817	473	2	US-08-477-733B-16	Sequence 16, Appli
745	23	100.0	451	4	US-10-113-996-18	Sequence 18, Appli	818	473	2	US-09-088-913A-16	Sequence 16, Appli
746	23	100.0	451	4	US-09-596-288-230	Sequence 230, App	819	473	3	US-09-049-672A-4	Sequence 4, Appli
747	23	100.0	452	3	US-09-027-449-71	Sequence 71, Appli	820	473	3	US-08-769-819-16	Sequence 16, Appli
748	23	100.0	452	3	US-09-026-985-71	Sequence 71, Appli	821	473	3	US-08-770-974-16	Sequence 16, Appli
749	23	100.0	452	4	US-09-121-952A-71	Sequence 71, Appli	822	473	3	US-08-770-981-16	Sequence 16, Appli
750	23	100.0	452	4	US-09-234-340A-71	Sequence 71, Appli	823	473	4	US-09-399-106-16	Sequence 16, Appli
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755	23	100.0	453	4	US-09-532-856-6	Sequence 6, Appli	828	475	4	US-09-740-002-27	Sequence 27, Appli
756	23	100.0	453	4	US-09-252-991A-25795	Sequence 25795, A	829	475	4	US-09-252-991A-18928	Sequence 18928, A
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833	23	100.0	476	3	US-08-487-550-12	Sequence 12, Appl	906	23	100.0	525	4	US-09-499-846-8	Sequence 8, Appl
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874	23	100.0	497	4	US-09-499-846-10	Sequence 10, Appl	947	23	100.0	543	4	US-09-322-977-2	Sequence 2, Appl
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979 23 100.0 567 4 US-09-825-561A-16 Sequence 16, Appl
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981 23 100.0 567 4 US-09-773-877B-20 Sequence 20, Appl
982 23 100.0 571 4 US-09-746-359A-53 Sequence 53, Appl
983 23 100.0 574 4 US-09-252-991A-19455 Sequence 19455, A
984 23 100.0 574 4 US-09-600-991-2 Sequence 2, Appl
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986 23 100.0 577 4 US-09-873-637-2 Sequence 2, Appl
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990 23 100.0 580 4 US-09-252-991A-27245 Sequence 27245, A
991 23 100.0 580 4 US-08-311-731A-289 Sequence 289, App
992 23 100.0 581 4 US-08-311-731A-286 Sequence 286, App
993 23 100.0 585 4 US-08-937-067-9 Sequence 9, Appl
994 23 100.0 585 4 US-09-252-991A-31529 Sequence 31529, A
995 23 100.0 587 3 US-09-102-528-30 Sequence 30, Appl
996 23 100.0 588 4 US-09-601-777-2 Sequence 2, Appl
997 23 100.0 588 4 US-09-252-991A-23755 Sequence 23755, A
998 23 100.0 590 4 US-09-529-279-15 Sequence 15, Appl
999 23 100.0 590 4 US-10-158-895-15 Sequence 15, Appl
1000 23 100.0 591 4 US-09-252-991A-20951 Sequence 20951, A

ALIGNMENTS

RESULT 1
US-08-922-170B-8
; Sequence 8, Application US/08922170B
; Patent No. 5968822
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
; APPLICANT: Feinstein
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
; TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
; TITLE OF INVENTION: SAME IN TRANSFUSED CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
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; APPLICATION NUMBER: US/08/922,170B
; FILING DATE: 2 SEP 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 910/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-922-170B-8
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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 6 GQPR 9
RESULT 2
US-09-435-739-8
; Sequence 8, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 00/20454
; CURRENT APPLICATION NUMBER: US/09/435,739
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-435-739-8
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 6 GQPR 9
RESULT 3
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; Sequence 8, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/256,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-09-988-113-8

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 4

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; Patent No. 6242238
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, Craig Geoffrey
; APPLICANT: PARISH, Richard
; APPLICANT: HAMMORF, Brenton James
; APPLICANT: HULETT, Mark Darren
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING MAMMALIAN
; TITLE OF INVENTION: ENDOGLUCURONIDASE AND USES THEREFOR
; FILE REFERENCE: 032505-004
; CURRENT APPLICATION NUMBER: US/09/181,336A
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: AU PP0062
; EARLIER FILING DATE: 1997-10-28
; EARLIER APPLICATION NUMBER: AU PP0812
; EARLIER FILING DATE: 1997-12-09
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-181-336-1

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Best Local Similarity 100.0%; Pred. No. 65;
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QY 1 GQPR 4
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RESULT 5

US-09-252-586-21
; Sequence 21, Application US/09252586
; Patent No. 6387643
; GENERAL INFORMATION:
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Fairbanks, Michael B.
; APPLICANT: Mildner, Ana M.
; TITLE OF INVENTION: Human Platelet Heparanase Polypeptides,
; TITLE OF INVENTION: Polynucleotide Molecules That Encode Them, and Methods For
; TITLE OF INVENTION: the Identification of Compounds That Alter Heparanase
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn
; STREET: 301 Henrietta
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/252,586
; FILING DATE:
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6131.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-833-0974
; TELEFAX: 616-833-8897
; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-252-586-21

Query Match 100.0%; Score 23; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 6

US-09-261-855-3
; Sequence 3, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-261-855-3

Query Match 100.0%; Score 23; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 9 GQPR 12

RESULT 7

US-09-873-637-3
; Sequence 3, Application US/09873637
; Patent No. 6794151
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
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; ORGANISM: Mus musculus
US-09-873-637-3

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      ||||
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; Sequence 109, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,780C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-780C-110

Query Match      100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      ||||
        1 GQPR 4

RESULT 10
US-08-471-780C-111
; Sequence 111, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 11
US-08-467-282B-109
Sequence 109, Application US/08467282B
Patent No. 5800988
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 12
US-08-467-282B-110
Sequence 110, Application US/08467282B
Patent No. 5800988
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 13
US-08-467-282B-111
Sequence 111, Application US/08467282B
Patent No. 5800988
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

```

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunne
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: ER 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-109

Query Match          100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

Qy 1 GQPR 4
Db 1 GQPR 4

RESULT 15
US-08-471-282A-110
; Sequence 110, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:

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APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-282A-110

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 16
US-08-471-282A-111
Sequence 111, Application US/08471282A
Patent No. 5840853
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-282A-111
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4

RESULT 17
US-08-466-710C-109
Sequence 109, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-710C-109

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 18

US-08-466-710C-110
; Sequence 110, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-710C-110
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4
RESULT 19
US-08-466-710C-111
; Sequence 111, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-710C-110

US-08-466-710C-110
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-710C-111
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4
RESULT 20
US-08-466-739C-109
; Sequence 109, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 109:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-468-739C-109

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 21
US-08-468-739C-110
; Sequence 110, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-739C-110

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 22
US-08-468-739C-111
; Sequence 111, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-739C-111

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 23
US-09-293-769A-109
; Sequence 109, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
```

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 109:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-468-739C-109

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 21
US-08-468-739C-110
; Sequence 110, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-739C-110

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 22
US-08-468-739C-111
; Sequence 111, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-739C-111

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 23
US-09-293-769A-109
; Sequence 109, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
```

FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92402326.0
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Camelus sp.
US-09-293-769A-109

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 24

US-09-293-769A-110
; Sequence 110, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILIE
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92402326.0
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Camelus sp.
US-09-293-769A-110

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 25

US-09-293-769A-111
; Sequence 111, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILIE
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000

CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92402326.0
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Camelus sp.
US-09-293-769A-111

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 26

US-08-471-780C-115
; Sequence 115, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,780C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-471-780C-115

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 27

US-08-471-780C-116
 ; Sequence 116, Application US/08471780C
 ; Patent No. 5759808
 ; GENERAL INFORMATION:
 ; APPLICANT: Casterman, Cecile
 ; APPLICANT: Hamers, Raymond
 ; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 ; NUMBER OF SEQUENCES: 130
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,780C
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/106,944
 ; FILING DATE: 17-AUG-1993
 ; APPLICATION NUMBER: FR 92402326.0
 ; FILING DATE: 21-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 93401310.3
 ; FILING DATE: 21-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Potter, Jane E.R.
 ; REGISTRATION NUMBER: 33,332
 ; REFERENCE/DOCKET NUMBER: 04958.0008-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 116:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-471-780C-116

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 28

US-08-471-780C-117
 ; Sequence 117, Application US/08471780C
 ; Patent No. 5759808
 ; GENERAL INFORMATION:

; APPLICANT: Casterman, Cecile
 ; APPLICANT: Hamers, Raymond
 ; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 ; NUMBER OF SEQUENCES: 130
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,780C
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/106,944
 ; FILING DATE: 17-AUG-1993
 ; APPLICATION NUMBER: FR 92402326.0
 ; FILING DATE: 21-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 93401310.3
 ; FILING DATE: 21-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Potter, Jane E.R.
 ; REGISTRATION NUMBER: 33,332
 ; REFERENCE/DOCKET NUMBER: 04958.0008-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 117:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-471-780C-117

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 29

US-08-467-282B-115
 ; Sequence 115, Application US/08467282B
 ; Patent No. 5800988
 ; GENERAL INFORMATION:
 ; APPLICANT: Casterman, Cecile
 ; APPLICANT: Hamers, Raymond
 ; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 ; NUMBER OF SEQUENCES: 130
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/467,282B
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA: FR 93401310.3
/ APPLICATION NUMBER: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4400
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 115:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-467-282B-115

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 2 GQPR 5

RESULT 30
US-08-467-282B-116
/ Sequence 116, Application US/08467282B
/ Patent No. 5800988
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US 08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4400
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-467-282B-117

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-467-282B-116

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 2 GQPR 5

RESULT 31
US-08-467-282B-117
/ Sequence 117, Application US/08467282B
/ Patent No. 5800988
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/467,282B
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-467-282B-117

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db |||||
 2 GQPR 5

RESULT 32
US-08-471-282A-115
; Sequence 115, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-115

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 2 GQPR 5

RESULT 33
US-08-471-282A-116
; Sequence 116, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-282A-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 2 GQPR 5

RESULT 34
US-08-471-282A-117
; Sequence 117, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993

```
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-471-282A-117

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 35
US-08-466-710C-115
/ Sequence 115, Application US/084666710C
/ Patent No. 5874541
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,710C
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 115:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-471-282A-117

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 36
US-08-466-710C-116
/ Sequence 116, Application US/084666710C
/ Patent No. 5874541
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,710C
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-466-710C-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 37
US-08-466-710C-117
/ Sequence 117, Application US/084666710C
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/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-466-710C-115

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 36
US-08-466-710C-116
/ Sequence 116, Application US/084666710C
/ Patent No. 5874541
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,710C
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-466-710C-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 37
US-08-466-710C-117
/ Sequence 117, Application US/084666710C
```

```

; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-710C-117

```

```

Query Match      100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 GQPR 4
Db      2 GQPR 5

```

```

RESULT 38
US-08-468-739C-115
; Sequence 115, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-739C-115

```

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Query Match      100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GQPR 4
Db      2 GQPR 5

```

```

RESULT 39
US-08-468-739C-116
; Sequence 116, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.

```

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-116

Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 40

US-08-468-739C-117
Sequence 117, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944

FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-117

Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 41

US-09-293-769A-115
Sequence 115, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 115
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-293-769A-115

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 42

US-09-293-769A-116
Sequence 116, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 116
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-293-769A-116

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGPR 4
|
|
|
|
Db 2 QGPR 5

RESULT 43

US-09-293-769A-117
; Sequence 117, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92402326.0
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-769A-117

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGPR 4
|
|
|
|
Db 2 QGPR 5

RESULT 44

US-08-851-843A-194
; Sequence 194, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGPR 4
|
|
|
|
Db 15 QGPR 18

RESULT 45

US-08-974-549A-313
; Sequence 313, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

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/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA: US 08/851,843
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 313:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-974-549A-313

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 46
US-08-854-050-194
; Sequence 194, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 194:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-854-050-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 47
US-09-430-323-194
; Sequence 194, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
```

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;
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-430-323-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 48
US-09-402-181B-313
; Sequence 313, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
;

;
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausubus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 313:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-09-402-181B-313

Query Match 100.0%; Score 23; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 49
US-09-721-456-313
; Sequence 313, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
;

```

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-09-721-456-313

Query Match 100.0%; Score 23; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 50
US-08-708-893-1
Sequence 1, Application US/08708893
Patent No. 5760175
GENERAL INFORMATION:
APPLICANT: Golubev, Daniel B
APPLICANT: Chaihorsky, Alexander
TITLE OF INVENTION: PEPTIDE VACCINE TO PREVENT DEVELOPMENT OF
TITLE OF INVENTION: SEVERAL HERPES VIRUS INFECTIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Firm of Karl F. Ross, PC
STREET: 5676 Riverdale Ave.
CITY: Bronx
STATE: New York
COUNTRY: USA
ZIP: 10471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,893
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (718) 884-6600
TELEFAX: 718/601-1099
TELEX: 620428
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-708-893-1
Query Match 100.0%; Score 23; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 24 GQPR 27
RESULT 51
US-09-088-154-1
Sequence 1, Application US/09088154
Patent No. 6015566
GENERAL INFORMATION:
APPLICANT: Golubev, Daniel B
APPLICANT: Chaihorsky, Alexander
TITLE OF INVENTION: PEPTIDE VACCINE TO PREVENT DEVELOPMENT OF
TITLE OF INVENTION: SEVERAL HERPES VIRUS INFECTIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Firm of Karl F. Ross, PC
STREET: 5676 Riverdale Ave.
CITY: Bronx
STATE: New York
COUNTRY: USA
ZIP: 10471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,154
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/708,893
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (718) 884-6600
TELEFAX: 718/601-1099
TELEX: 620428
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO


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; ANTI-SENSE: NO
US-09-088-154-1
Query Match      100.0%; Score 23; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      24 GQPR 27

RESULT 52
US-08-809-440-16
; Sequence 16, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Tautsumi, No. 5929017iko
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5929017o No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5929017e
US-08-809-440-16

Query Match      100.0%; Score 23; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      18 GQPR 21

RESULT 53
US-09-523-686-2
; Sequence 2, Application US/09523686
; Patent No. 6518043
; GENERAL INFORMATION:
; APPLICANT: Oritani, Kenji
```

```
; APPLICANT: Tomiyama, Yoshiaki
; APPLICANT: Matsuzawa, Yuji
; APPLICANT: Paul W. Kincade
; TITLE OF INVENTION: Proteins Suppressing proliferation of lympho-hematopoietic cells
; FILE REFERENCE: SEN-103-US
; CURRENT APPLICATION NUMBER: US/09/523,686
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: JP 1999-107246
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-523-686-2

Query Match      100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      13 GQPR 16

RESULT 54
US-10-038-612-70
; Sequence 70, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short peptides which selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 35
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: TrkC
US-10-038-612-70

Query Match      100.0%; Score 23; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      26 GQPR 29

RESULT 55
US-09-461-325-262
; Sequence 262, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
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; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G3OAP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-115-123-262

Query Match 100.0%; Score 23; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 16 GQPR 19

RESULT 58
US-08-809-440-15
; Sequence 15, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Teitsumi, No. 5929017iko
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5929017o No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 15:

```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5929017e
US-08-809-440-15

Query Match 100.0%; Score 23; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 34 GQPR 37

RESULT 59
US-08-548-540-94
; Sequence 94, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09809
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,540
; FILING DATE: 26-OCT-1995
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-09809-94

Query Match 100.0%; Score 23; DB 5; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 25 GQPR 28

RESULT 61
US-08-488-161-66
; Sequence 66, Application US/08488161
; Patent No. 5865577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-161-66

Query Match 100.0%; Score 23; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 62
US-09-273-685-66
Sequence 66, Application US/09273685
Patent No. 6015561
GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
REFERENCE/DOCKET NUMBER: 1101-176
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/488,161
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-273-685-66

Query Match 100.0%; Score 23; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 63
PCT-US95-11934-66
Sequence 66, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
REFERENCE/DOCKET NUMBER: 1101-196-228
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11934-66

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 64

US-08-548-540-93
; Sequence 93, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-548-540-93

Query Match 100.0%; Score 23; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 26 GQPR 29

RESULT 65
PCT-US96-09809-93
; Sequence 93, Application PC/TUS9609809
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,540
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528J-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-09809-93

Query Match 100.0%; Score 23; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 26 GQPR 29

RESULT 66
US-08-809-440-17
; Sequence 17, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Teutsumi, No. 5929017iko
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5929017o.No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997

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; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5929017e
US-08-809-440-17

Query Match 100.0%; Score 23; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 34 GQPR 37

RESULT 67
US-09-434-840-65
; Sequence 65, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jirage, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feys, Bart
; TITLE OF INVENTION: PAPA COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Rhizomucor miehei
US-09-434-840-65

Query Match 100.0%; Score 23; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 20 GQPR 23

RESULT 68
US-09-270-767-42207
; Sequence 42207, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42207
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; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42207

Query Match 100.0%; Score 23; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 32 GQPR 35

RESULT 69
US-09-270-767-60731
; Sequence 60731, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60731
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60731

Query Match 100.0%; Score 23; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 25 GQPR 28

RESULT 70
US-09-489-039A-8043
; Sequence 8043, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8043
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8043

Query Match 100.0%; Score 23; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 21 GQPR 24

RESULT 71
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US-09-248-796A-27059
; Sequence 27059, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27059
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27059

Query Match 100.0%; Score 23; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 48 GQPR 51

RESULT 72
US-08-754-477A-139
; Sequence 139, Application US/08754477A
; Patent No. 6518411
; GENERAL INFORMATION:
; APPLICANT: Murray, Jeffrey
; APPLICANT: Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,477A
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-022.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-754-477A-139

Query Match 100.0%; Score 23; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 42 GQPR 45

RESULT 73
US-09-227-357-163
; Sequence 163, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954

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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-227-357-163

Query Match      100.0%; Score 23; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
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Db      55 GQPR 58

RESULT 74
US-09-270-767-32321
; Sequence 32321, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32321
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32321

Query Match      100.0%; Score 23; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
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Db      48 GQPR 51

RESULT 75
US-09-270-767-47538
; Sequence 47538, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47538
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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US-09-270-767-47538

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Query Match      100.0%; Score 23; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GQPR 4
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Db      48 GQPR 51
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Search completed: May 17, 2005, 10:08:24
Job time : 34 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2005, 10:04:26 ; Search time 136 Seconds
(without alignments)
9.825 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Published Applications, AA:*

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- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	4	14	US-10-197-954-120
2	23	100.0	4	16	US-10-742-344-3
3	23	100.0	4	16	US-10-731-921-3
4	23	100.0	4	17	US-10-760-085-120
5	23	100.0	9	9	US-09-776-874A-8
6	23	100.0	9	9	US-09-988-113-8
7	23	100.0	9	14	US-10-341-582-8
8	23	100.0	9	14	US-10-384-451-8
9	23	100.0	9	14	US-10-384-450-8
10	23	100.0	9	15	US-10-371-218A-8
11	23	100.0	9	15	US-10-456-573-8
12	23	100.0	9	16	US-10-785-116-8
13	23	100.0	12	11	US-09-920-306-63
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15	23	100.0	14	9	US-09-873-637-3	Sequence 3, Appli
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17	23	100.0	17	9	US-09-984-017-2	Sequence 2, Appli
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19	23	100.0	20	9	US-09-843-676-194	Sequence 194, App
20	23	100.0	20	10	US-09-438-486-194	Sequence 194, App
21	23	100.0	20	14	US-10-053-758-194	Sequence 194, App
22	23	100.0	20	14	US-10-054-295-194	Sequence 194, App
23	23	100.0	20	14	US-10-054-611-194	Sequence 194, App
24	23	100.0	20	15	US-10-325-810-313	Sequence 313, App
25	23	100.0	20	17	US-10-877-146-313	Sequence 313, App
26	23	100.0	22	14	US-10-263-162-45	Sequence 15, Appl
27	23	100.0	23	15	US-10-384-060-15	Sequence 15, Appl
28	23	100.0	26	10	US-09-847-102A-119	Sequence 119, App
29	23	100.0	27	10	US-09-820-843A-81	Sequence 81, Appl
30	23	100.0	31	14	US-10-029-386-28116	Sequence 28116, A
31	23	100.0	33	14	US-10-295-732-2	Sequence 2, Appli
32	23	100.0	34	16	US-10-437-963-130130	Sequence 130130,
33	23	100.0	35	13	US-10-038-612-70	Sequence 70, Appl
34	23	100.0	35	14	US-10-231-417-404	Sequence 404, App
35	23	100.0	36	10	US-09-104-750-50	Sequence 50, Appl
36	23	100.0	36	16	US-10-437-963-108727	Sequence 108727,
37	23	100.0	36	16	US-10-767-701-61720	Sequence 61720, A
38	23	100.0	37	14	US-10-012-542-262	Sequence 262, App
39	23	100.0	37	14	US-10-115-123-262	Sequence 262, App
40	23	100.0	38	10	US-09-776-724A-227	Sequence 227, App
41	23	100.0	38	16	US-10-437-963-152267	Sequence 152267,
42	23	100.0	40	16	US-10-437-963-151924	Sequence 151924,
43	23	100.0	41	9	US-09-864-761-45995	Sequence 45995, A
44	23	100.0	41	15	US-10-240-145-162	Sequence 162, App
45	23	100.0	42	15	US-10-424-599-145097	Sequence 145097,
46	23	100.0	44	15	US-10-424-599-177895	Sequence 177895,
47	23	100.0	44	15	US-10-424-599-255629	Sequence 255629,
48	23	100.0	46	9	US-09-864-761-38712	Sequence 38712, A
49	23	100.0	46	16	US-10-437-963-139079	Sequence 139079,
50	23	100.0	49	9	US-09-864-761-45670	Sequence 45670, A
51	23	100.0	50	11	US-09-864-408A-8876	Sequence 8876, Ap
52	23	100.0	51	14	US-10-091-007-26	Sequence 26, Appl
53	23	100.0	51	15	US-10-424-599-185208	Sequence 185208,
54	23	100.0	52	15	US-10-424-599-180797	Sequence 180797,
55	23	100.0	52	15	US-10-424-599-247027	Sequence 247027,
56	23	100.0	53	15	US-10-424-599-170629	Sequence 170629,
57	23	100.0	54	15	US-10-424-599-151840	Sequence 151840,
58	23	100.0	55	14	US-10-029-386-34129	Sequence 34129, A
59	23	100.0	57	16	US-10-437-963-155414	Sequence 155414,
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61	23	100.0	59	15	US-10-424-599-181996	Sequence 181996,
62	23	100.0	60	15	US-10-424-599-145320	Sequence 145320,
63	23	100.0	60	15	US-10-424-599-155931	Sequence 155931,
64	23	100.0	60	15	US-10-424-599-155931	Sequence 155931,
65	23	100.0	62	11	US-09-864-408A-5620	Sequence 5620, Ap
66	23	100.0	63	15	US-10-424-599-177632	Sequence 177632,
67	23	100.0	63	15	US-10-424-599-233719	Sequence 233719,
68	23	100.0	64	16	US-10-437-963-163011	Sequence 163011,
69	23	100.0	65	16	US-10-437-963-155904	Sequence 155904,
70	23	100.0	67	16	US-10-437-963-104594	Sequence 104594,
71	23	100.0	68	11	US-09-864-408A-6184	Sequence 6184, Ap
72	23	100.0	68	14	US-10-105-004-139	Sequence 139, App
73	23	100.0	69	16	US-10-437-963-106825	Sequence 106825,
74	23	100.0	70	15	US-10-424-599-143493	Sequence 143493,
75	23	100.0	70	15	US-10-424-599-211412	Sequence 211412,
76	23	100.0	71	15	US-09-764-891-2702	Sequence 2702, Ap
77	23	100.0	71	15	US-10-424-599-219870	Sequence 219870,
78	23	100.0	71	16	US-10-437-963-169344	Sequence 169344,
79	23	100.0	72	14	US-10-029-386-72315	Sequence 72315, A
80	23	100.0	72	15	US-10-424-599-189369	Sequence 189369,
81	23	100.0	73	15	US-10-424-599-148374	Sequence 148374,
82	23	100.0	73	15	US-10-424-599-155441	Sequence 155441,
83	23	100.0	73	15	US-10-424-599-245639	Sequence 245639,
84	23	100.0	74	9	US-09-789-561-124	Sequence 124, App
85	23	100.0	74	10	US-09-983-802-163	Sequence 163, App
86	23	100.0	74	10	US-09-984-490-163	Sequence 163, App

87	23	100.0	74	11	US-09-833-245-2128	Sequence 2128, Ap	160	23	100.0	100	16	US-10-437-963-147030	Sequence 147030,
88	23	100.0	74	11	US-09-973-278-206	Sequence 206, App	161	23	100.0	100	16	US-10-437-963-160978	Sequence 160978,
89	23	100.0	74	14	US-10-029-386-28857	Sequence 28857, A	162	23	100.0	100	16	US-10-437-963-162749	Sequence 162749,
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91	23	100.0	74	16	US-10-437-963-173930	Sequence 173930,	164	23	100.0	101	16	US-10-437-963-138801	Sequence 138801,
92	23	100.0	74	16	US-10-437-963-196719	Sequence 196719,	165	23	100.0	102	15	US-10-104-047-3923	Sequence 3923, Ap
93	23	100.0	74	17	US-10-883-936-124	Sequence 124, App	166	23	100.0	102	15	US-10-424-599-143920	Sequence 143920,
94	23	100.0	75	15	US-10-424-599-156672	Sequence 156672,	167	23	100.0	102	15	US-10-424-599-154941	Sequence 154941,
95	23	100.0	75	15	US-10-425-114-70336	Sequence 70336, A	168	23	100.0	102	15	US-10-424-599-194109	Sequence 194109,
96	23	100.0	75	16	US-10-437-963-152229	Sequence 152229,	169	23	100.0	102	15	US-10-424-599-216941	Sequence 216941,
97	23	100.0	75	16	US-10-437-963-171622	Sequence 171622,	170	23	100.0	102	15	US-10-424-599-240595	Sequence 240595,
98	23	100.0	75	16	US-10-437-963-172136	Sequence 172136,	171	23	100.0	103	16	US-10-424-599-231032	Sequence 231032,
99	23	100.0	76	15	US-10-424-599-236220	Sequence 236220,	172	23	100.0	103	16	US-10-437-963-121650	Sequence 121650,
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101	23	100.0	76	16	US-10-437-963-174737	Sequence 174737,	174	23	100.0	105	16	US-10-424-599-161374	Sequence 161374,
102	23	100.0	77	11	US-09-864-408A-6800	Sequence 6800, Ap	175	23	100.0	105	16	US-10-437-963-155376	Sequence 155376,
103	23	100.0	78	16	US-10-437-963-145755	Sequence 145755,	176	23	100.0	105	16	US-10-437-963-163883	Sequence 163883,
104	23	100.0	78	16	US-10-437-963-183354	Sequence 183354,	177	23	100.0	106	15	US-10-424-599-188365	Sequence 188365,
105	23	100.0	78	16	US-10-767-701-60411	Sequence 60411, A	178	23	100.0	106	16	US-10-437-963-163584	Sequence 163584,
106	23	100.0	79	15	US-10-424-599-179326	Sequence 179326,	179	23	100.0	106	16	US-10-437-963-164863	Sequence 164863,
107	23	100.0	80	16	US-10-437-963-145218	Sequence 145218,	180	23	100.0	107	14	US-10-267-286A-5	Sequence 5, Appli
108	23	100.0	80	16	US-10-437-963-169341	Sequence 169341,	181	23	100.0	107	14	US-10-207-655-222	Sequence 222, App
109	23	100.0	80	16	US-10-437-963-173391	Sequence 173391,	182	23	100.0	107	14	US-10-207-655-375	Sequence 375, App
110	23	100.0	80	16	US-10-767-701-54726	Sequence 54726, A	183	23	100.0	107	14	US-10-207-655-376	Sequence 376, App
111	23	100.0	81	15	US-10-424-599-148176	Sequence 148176,	184	23	100.0	107	14	US-10-207-655-377	Sequence 377, App
112	23	100.0	81	15	US-10-424-599-234140	Sequence 234140,	185	23	100.0	107	14	US-10-207-655-378	Sequence 378, App
113	23	100.0	82	11	US-09-833-245-196	Sequence 196, App	186	23	100.0	107	14	US-10-207-655-379	Sequence 379, App
114	23	100.0	82	14	US-10-029-386-28922	Sequence 28922, A	187	23	100.0	107	15	US-10-370-749-24	Sequence 24, Appl
115	23	100.0	82	15	US-10-424-599-191577	Sequence 191577,	188	23	100.0	107	15	US-10-264-049-2368	Sequence 2368, Ap
116	23	100.0	82	15	US-10-425-000-93	Sequence 93, Appl	189	23	100.0	107	15	US-10-424-599-208487	Sequence 208487,
117	23	100.0	82	15	US-10-424-999-58	Sequence 58, Appl	190	23	100.0	107	15	US-10-425-114-40171	Sequence 40171, A
118	23	100.0	82	16	US-10-767-701-42420	Sequence 42420, A	191	23	100.0	107	16	US-10-307-276B-46	Sequence 46, Appl
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121	23	100.0	84	16	US-10-437-963-164940	Sequence 164940,	194	23	100.0	107	16	US-10-437-963-134747	Sequence 134747,
122	23	100.0	85	15	US-10-424-599-247618	Sequence 247618,	195	23	100.0	107	16	US-10-684-109-74	Sequence 74, Appl
123	23	100.0	86	10	US-09-764-872-407	Sequence 407, App	196	23	100.0	107	17	US-10-491-653-6	Sequence 6, Appli
124	23	100.0	86	16	US-10-767-701-32827	Sequence 32827, A	197	23	100.0	108	9	US-09-864-761-42141	Sequence 42141, A
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126	23	100.0	87	9	US-09-764-868-1134	Sequence 1134, Ap	199	23	100.0	108	15	US-10-424-599-251295	Sequence 251295,
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132	23	100.0	89	16	US-10-408-765A-780	Sequence 780, App	205	23	100.0	109	16	US-10-437-963-177648	Sequence 177648,
133	23	100.0	89	16	US-10-408-765A-781	Sequence 781, App	206	23	100.0	110	14	US-10-029-386-29859	Sequence 29859, A
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139	23	100.0	92	14	US-10-106-698-8371	Sequence 8371, Ap	212	23	100.0	112	15	US-10-424-599-165610	Sequence 165610,
140	23	100.0	92	16	US-10-437-963-123359	Sequence 123359,	213	23	100.0	112	15	US-09-922-226-129	Sequence 129, App
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142	23	100.0	93	16	US-10-767-701-36878	Sequence 36878, A	215	23	100.0	113	15	US-10-424-599-171969	Sequence 171969,
143	23	100.0	94	15	US-10-264-049-2545	Sequence 2545, Ap	216	23	100.0	113	16	US-10-437-963-125572	Sequence 125572,
144	23	100.0	94	16	US-10-437-963-107682	Sequence 107682,	217	23	100.0	114	9	US-09-864-761-42278	Sequence 42278, A
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148	23	100.0	96	15	US-10-424-599-191513	Sequence 191513,	221	23	100.0	115	15	US-10-424-599-223544	Sequence 223544,
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151	23	100.0	97	16	US-10-437-963-193790	Sequence 193790,	224	23	100.0	117	9	US-09-925-301-1554	Sequence 1554, Ap
152	23	100.0	98	15	US-10-424-599-250537	Sequence 250537,	225	23	100.0	117	16	US-10-437-963-116438	Sequence 116438,
153	23	100.0	98	15	US-10-424-599-270892	Sequence 270892,	226	23	100.0	118	15	US-10-424-599-171957	Sequence 171957,
154	23	100.0	98	15	US-10-425-114-60729	Sequence 60729, A	227	23	100.0	118	16	US-10-437-963-138829	Sequence 138829,
155	23	100.0	98	16	US-10-437-963-196738	Sequence 196738,	228	23	100.0	118	16	US-10-437-963-202851	Sequence 202851,
156	23	100.0	98	16	US-10-767-701-53395	Sequence 53395, A	229	23	100.0	119	16	US-10-437-963-103120	Sequence 103120,
157	23	100.0	99	16	US-10-437-963-141929	Sequence 141929,	230	23	100.0	119	16	US-10-437-963-127851	Sequence 127851,
158	23	100.0	100	15	US-10-276-774-2312	Sequence 2312, Ap	231	23	100.0	120	15	US-10-108-260A-3510	Sequence 3510, Ap
159	23	100.0	100	16	US-10-437-963-138859	Sequence 138859,	232	23	100.0	120	16	US-10-437-963-163722	Sequence 163722,

233	23	100.0	120	16	US-10-767-701-46585	Sequence 46585, A	306	23	100.0	148	16	US-10-437-963-114731	Sequence 114731,
234	23	100.0	120	16	US-10-767-701-53752	Sequence 53752, A	307	23	100.0	149	9	US-09-764-847-517	Sequence 517, App
235	23	100.0	121	16	US-10-437-963-131318	Sequence 131318, A	308	23	100.0	149	14	US-10-092-154-517	Sequence 32381, A
236	23	100.0	121	16	US-10-437-963-140181	Sequence 140181, A	309	23	100.0	150	16	US-10-767-701-32381	Sequence 32381, A
237	23	100.0	122	16	US-09-925-299-1161	Sequence 1161, App	310	23	100.0	150	16	US-10-767-701-37105	Sequence 37105, A
238	23	100.0	123	9	US-09-925-299-1161	Sequence 1161, App	311	23	100.0	150	16	US-10-767-701-44536	Sequence 44536, A
239	23	100.0	123	16	US-10-437-963-140955	Sequence 140955, A	312	23	100.0	151	16	US-10-437-963-115199	Sequence 115199, A
240	23	100.0	124	16	US-10-437-963-176651	Sequence 176651, A	313	23	100.0	151	16	US-10-437-963-115199	Sequence 115199, A
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243	23	100.0	126	14	US-10-277-726A-15	Sequence 189234, A	316	23	100.0	152	14	US-10-029-386-32515	Sequence 32515, A
244	23	100.0	126	15	US-10-425-114-50397	Sequence 15, Appl	317	23	100.0	152	14	US-10-437-963-131079	Sequence 131079, A
245	23	100.0	127	11	US-09-973-278-251	Sequence 50397, A	318	23	100.0	152	16	US-10-767-701-62408	Sequence 62408, A
246	23	100.0	127	11	US-09-973-278-251	Sequence 251, App	319	23	100.0	152	16	US-10-767-701-62408	Sequence 62408, A
247	23	100.0	127	15	US-10-411-120-87	Sequence 87, Appl	320	23	100.0	153	15	US-10-767-701-66790	Sequence 66790, A
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249	23	100.0	127	15	US-10-424-599-254333	Sequence 254333, A	322	23	100.0	153	16	US-10-437-963-120683	Sequence 120683, A
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251	23	100.0	128	10	US-09-984-490-130	Sequence 190, App	324	23	100.0	154	16	US-10-767-701-44627	Sequence 44627, A
252	23	100.0	128	16	US-10-437-963-135226	Sequence 135226, A	325	23	100.0	155	15	US-09-975-456B-10	Sequence 10, Appl
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254	23	100.0	128	16	US-10-437-963-194034	Sequence 194034, A	327	23	100.0	156	15	US-10-767-701-35901	Sequence 35901, A
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395	23	100.0	180	9	US-09-854-208-1	Sequence 1, Appl	468	180	14	US-10-124-822-446	Sequence 446, App
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398	23	100.0	180	9	US-09-874-503-2	Sequence 2, Appl	471	180	14	US-10-124-824-446	Sequence 446, App
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434	23	100.0	180	11	US-09-796-844-35	Sequence 35, Appl	507	180	14	US-10-152-395-446	Sequence 446, App
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439	23	100.0	180	14	US-10-123-904-446	Sequence 446, App	512	180	14	US-10-127-838B-446	Sequence 446, App
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448	23	100.0	180	14	US-10-142-419-446	Sequence 446, App	521	180	14	US-10-128-684A-446	Sequence 446, App
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529	23	100.0	180	14	US-10-146-791-446	Sequence 446, App	602	23	100.0	180	14	US-10-144-994-446	Sequence 446, App
530	23	100.0	180	14	US-10-147-484-446	Sequence 446, App	603	23	100.0	180	14	US-10-145-628-446	Sequence 446, App
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543	23	100.0	180	14	US-10-123-907-446	Sequence 446, App	616	23	100.0	180	14	US-10-147-504-446	Sequence 446, App
544	23	100.0	180	14	US-10-124-815-446	Sequence 446, App	617	23	100.0	180	14	US-10-147-506-446	Sequence 446, App
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546	23	100.0	180	14	US-10-125-928A-446	Sequence 446, App	619	23	100.0	180	14	US-10-147-510-446	Sequence 446, App
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548	23	100.0	180	14	US-10-127-822A-446	Sequence 446, App	621	23	100.0	180	14	US-10-147-529-446	Sequence 446, App
549	23	100.0	180	14	US-10-127-824A-446	Sequence 446, App	622	23	100.0	180	14	US-10-152-397-446	Sequence 446, App
550	23	100.0	180	14	US-10-127-833A-446	Sequence 446, App	623	23	100.0	180	14	US-10-153-586-446	Sequence 446, App
551	23	100.0	180	14	US-10-127-827A-446	Sequence 446, App	624	23	100.0	180	14	US-10-158-786-446	Sequence 446, App
552	23	100.0	180	14	US-10-127-828A-446	Sequence 446, App	625	23	100.0	180	14	US-10-143-031A-470	Sequence 470, App
553	23	100.0	180	14	US-10-127-830A-446	Sequence 446, App	626	23	100.0	180	14	US-10-137-870-446	Sequence 446, App
554	23	100.0	180	14	US-10-127-832A-446	Sequence 446, App	627	23	100.0	180	14	US-10-140-018-446	Sequence 446, App
555	23	100.0	180	14	US-10-127-833A-446	Sequence 446, App	628	23	100.0	180	14	US-10-140-021-446	Sequence 446, App
556	23	100.0	180	14	US-10-127-834A-446	Sequence 446, App	629	23	100.0	180	14	US-10-140-071-446	Sequence 446, App
557	23	100.0	180	14	US-10-127-836A-446	Sequence 446, App	630	23	100.0	180	14	US-10-140-922-446	Sequence 446, App
558	23	100.0	180	14	US-10-127-841A-446	Sequence 446, App	631	23	100.0	180	14	US-10-145-631-446	Sequence 446, App
559	23	100.0	180	14	US-10-127-844A-446	Sequence 446, App	632	23	100.0	180	14	US-10-145-633-446	Sequence 446, App
560	23	100.0	180	14	US-10-128-687A-446	Sequence 446, App	633	23	100.0	180	14	US-10-158-783-446	Sequence 446, App
561	23	100.0	180	14	US-10-128-688A-446	Sequence 446, App	634	23	100.0	180	14	US-10-340-042-2	Sequence 2, Appli
562	23	100.0	180	14	US-10-128-689A-446	Sequence 446, App	635	23	100.0	180	14	US-10-140-274-446	Sequence 446, App
563	23	100.0	180	14	US-10-128-694A-446	Sequence 446, App	636	23	100.0	180	14	US-10-143-030A-470	Sequence 470, App
564	23	100.0	180	14	US-10-131-825A-446	Sequence 446, App	637	23	100.0	180	14	US-10-002-967A-470	Sequence 470, App
565	23	100.0	180	14	US-10-230-417-446	Sequence 446, App	638	23	100.0	180	14	US-10-017-083A-470	Sequence 470, App
566	23	100.0	180	14	US-10-131-815A-446	Sequence 446, App	639	23	100.0	180	14	US-10-140-019-446	Sequence 446, App
567	23	100.0	180	14	US-10-131-817A-446	Sequence 446, App	640	23	100.0	180	14	US-10-140-022-446	Sequence 446, App
568	23	100.0	180	14	US-10-131-821A-446	Sequence 446, App	641	23	100.0	180	14	US-10-140-861-446	Sequence 446, App
569	23	100.0	180	14	US-10-131-822A-446	Sequence 446, App	642	23	100.0	180	14	US-10-140-862-446	Sequence 446, App
570	23	100.0	180	14	US-10-131-828A-446	Sequence 446, App	643	23	100.0	180	14	US-10-141-697-446	Sequence 446, App
571	23	100.0	180	14	US-10-131-835A-446	Sequence 446, App	644	23	100.0	180	14	US-10-141-700-446	Sequence 446, App
572	23	100.0	180	14	US-10-137-864A-446	Sequence 446, App	645	23	100.0	180	14	US-10-141-705-446	Sequence 446, App
573	23	100.0	180	14	US-10-137-869A-446	Sequence 446, App	646	23	100.0	180	14	US-10-141-753-446	Sequence 446, App
574	23	100.0	180	14	US-10-147-523-446	Sequence 446, App	647	23	100.0	180	14	US-10-141-758-446	Sequence 446, App
575	23	100.0	180	14	US-10-158-785-446	Sequence 446, App	648	23	100.0	180	14	US-10-142-418-446	Sequence 446, App
576	23	100.0	180	14	US-10-153-770-8	Sequence 8, Appli	649	23	100.0	180	14	US-10-142-420-446	Sequence 446, App
577	23	100.0	180	14	US-10-121-051-446	Sequence 446, App	650	23	100.0	180	14	US-10-142-422-446	Sequence 446, App
578	23	100.0	180	14	US-10-121-042-446	Sequence 446, App	651	23	100.0	180	14	US-10-142-427-446	Sequence 446, App
579	23	100.0	180	14	US-10-123-912-446	Sequence 446, App	652	23	100.0	180	14	US-10-142-760-446	Sequence 446, App
580	23	100.0	180	14	US-10-166-709A-470	Sequence 470, App	653	23	100.0	180	14	US-10-145-821-446	Sequence 446, App
581	23	100.0	180	14	US-10-192-007-446	Sequence 446, App	654	23	100.0	180	14	US-10-152-531-446	Sequence 446, App
582	23	100.0	180	14	US-10-194-359-446	Sequence 446, App	655	23	100.0	180	14	US-10-127-840A-446	Sequence 446, App
583	23	100.0	180	14	US-10-253-159-2	Sequence 2, Appli	656	23	100.0	180	14	US-10-142-424-446	Sequence 446, App
584	23	100.0	180	14	US-10-156-761-11409	Sequence 11409, A	657	23	100.0	180	14	US-10-142-761-446	Sequence 446, App
585	23	100.0	180	14	US-10-127-847A-446	Sequence 446, App	658	23	100.0	180	14	US-10-142-763-446	Sequence 446, App
586	23	100.0	180	14	US-10-137-866-446	Sequence 446, App	659	23	100.0	180	14	US-10-142-765-446	Sequence 446, App
587	23	100.0	180	14	US-10-146-726-446	Sequence 446, App	660	23	100.0	180	14	US-10-142-887-446	Sequence 446, App
588	23	100.0	180	14	US-10-146-727-446	Sequence 446, App	661	23	100.0	180	14	US-10-142-888-446	Sequence 446, App
589	23	100.0	180	14	US-10-146-788-446	Sequence 446, App	662	23	100.0	180	14	US-10-143-034-446	Sequence 446, App
590	23	100.0	180	14	US-10-152-380-446	Sequence 446, App	663	23	100.0	180	14	US-10-143-116-446	Sequence 446, App
591	23	100.0	180	14	US-10-153-934-446	Sequence 446, App	664	23	100.0	180	14	US-10-144-957-446	Sequence 446, App
592	23	100.0	180	14	US-10-140-807-446	Sequence 446, App	665	23	100.0	180	14	US-10-144-992-446	Sequence 446, App
593	23	100.0	180	14	US-10-140-924-446	Sequence 446, App	666	23	100.0	180	14	US-10-145-015-446	Sequence 446, App
594	23	100.0	180	14	US-10-140-926-446	Sequence 446, App	667	23	100.0	180	14	US-10-145-090-446	Sequence 446, App
595	23	100.0	180	14	US-10-141-698-446	Sequence 446, App	668	23	100.0	180	14	US-10-145-091-446	Sequence 446, App
596	23	100.0	180	14	US-10-141-702-446	Sequence 446, App	669	23	100.0	180	14	US-10-145-138A-470	Sequence 470, App
597	23	100.0	180	14	US-10-141-704-446	Sequence 446, App	670	23	100.0	180	14	US-10-145-629-446	Sequence 446, App

671	23	100.0	180	14	US-10-145-630-446	Sequence 446, App	744	23	100.0	180	14	US-10-145-960-446	Sequence 446, App
672	23	100.0	180	14	US-10-145-747-446	Sequence 446, App	745	23	100.0	180	14	US-10-145-962-446	Sequence 446, App
673	23	100.0	180	14	US-10-145-752-446	Sequence 446, App	746	23	100.0	180	14	US-10-146-789-446	Sequence 446, App
674	23	100.0	180	14	US-10-145-754-446	Sequence 446, App	747	23	100.0	180	14	US-10-147-433-446	Sequence 446, App
675	23	100.0	180	14	US-10-145-755-446	Sequence 446, App	748	23	100.0	180	14	US-10-147-496-446	Sequence 446, App
676	23	100.0	180	14	US-10-145-818-446	Sequence 446, App	749	23	100.0	180	14	US-10-147-505-446	Sequence 446, App
677	23	100.0	180	14	US-10-145-820-446	Sequence 446, App	750	23	100.0	180	14	US-10-147-516-446	Sequence 446, App
678	23	100.0	180	14	US-10-145-872-446	Sequence 446, App	751	23	100.0	180	14	US-10-152-398-446	Sequence 446, App
679	23	100.0	180	14	US-10-145-873-446	Sequence 446, App	752	23	100.0	180	14	US-10-277-726A-2	Sequence 2, Appli
680	23	100.0	180	14	US-10-147-481-446	Sequence 446, App	753	23	100.0	180	14	US-10-139-980-446	Sequence 446, App
681	23	100.0	180	14	US-10-147-482-446	Sequence 446, App	754	23	100.0	180	14	US-10-165-967A-470	Sequence 470, App
682	23	100.0	180	14	US-10-147-503-446	Sequence 446, App	755	23	100.0	180	14	US-10-410-374-2	Sequence 2, Appli
683	23	100.0	180	14	US-10-147-522-446	Sequence 446, App	756	23	100.0	180	14	US-10-145-017A-470	Sequence 470, App
684	23	100.0	180	14	US-10-153-401-446	Sequence 446, App	757	23	100.0	180	14	US-10-145-770-446	Sequence 446, App
685	23	100.0	180	14	US-10-157-783-446	Sequence 446, App	758	23	100.0	180	14	US-10-152-373-446	Sequence 446, App
686	23	100.0	180	14	US-10-158-792-446	Sequence 446, App	759	23	100.0	180	14	US-10-164-728A-470	Sequence 470, App
687	23	100.0	180	14	US-10-158-462-446	Sequence 446, App	760	23	100.0	180	14	US-10-397-282-8	Sequence 8, Appli
688	23	100.0	180	14	US-10-143-035-446	Sequence 446, App	761	23	100.0	180	14	US-10-013-926A-470	Sequence 470, App
689	23	100.0	180	14	US-10-145-751-446	Sequence 446, App	762	23	100.0	180	14	US-10-165-247A-470	Sequence 470, App
690	23	100.0	180	14	US-10-145-822-446	Sequence 446, App	763	23	100.0	180	14	US-10-145-124A-470	Sequence 470, App
691	23	100.0	180	14	US-10-145-824-446	Sequence 446, App	764	23	100.0	180	14	US-10-160-502A-470	Sequence 470, App
692	23	100.0	180	14	US-10-145-827-446	Sequence 446, App	765	23	100.0	180	14	US-10-121-044-446	Sequence 446, App
693	23	100.0	180	14	US-10-145-869-446	Sequence 446, App	766	23	100.0	180	14	US-10-121-055-446	Sequence 446, App
694	23	100.0	180	14	US-10-145-875-446	Sequence 446, App	767	23	100.0	180	14	US-10-121-057-446	Sequence 446, App
695	23	100.0	180	14	US-10-145-877-446	Sequence 446, App	768	23	100.0	180	14	US-10-121-058-446	Sequence 446, App
696	23	100.0	180	14	US-10-145-958-446	Sequence 446, App	769	23	100.0	180	14	US-10-121-059-446	Sequence 446, App
697	23	100.0	180	14	US-10-146-787-446	Sequence 446, App	770	23	100.0	180	14	US-10-121-060-446	Sequence 446, App
698	23	100.0	180	14	US-10-146-790-446	Sequence 446, App	771	23	100.0	180	14	US-10-123-109-446	Sequence 446, App
699	23	100.0	180	14	US-10-146-793-446	Sequence 446, App	772	23	100.0	180	14	US-10-123-154-446	Sequence 446, App
700	23	100.0	180	14	US-10-147-480-446	Sequence 446, App	773	23	100.0	180	14	US-10-123-157-446	Sequence 446, App
701	23	100.0	180	14	US-10-147-485-446	Sequence 446, App	774	23	100.0	180	14	US-10-123-906-446	Sequence 446, App
702	23	100.0	180	14	US-10-147-486-446	Sequence 446, App	775	23	100.0	180	14	US-10-124-814-446	Sequence 446, App
703	23	100.0	180	14	US-10-147-487-446	Sequence 446, App	776	23	100.0	180	14	US-10-124-816-446	Sequence 446, App
704	23	100.0	180	14	US-10-147-490-446	Sequence 446, App	777	23	100.0	180	14	US-10-124-820-446	Sequence 446, App
705	23	100.0	180	14	US-10-147-494-446	Sequence 446, App	778	23	100.0	180	14	US-10-125-704-446	Sequence 446, App
706	23	100.0	180	14	US-10-147-498-446	Sequence 446, App	779	23	100.0	180	14	US-10-125-927-446	Sequence 446, App
707	23	100.0	180	14	US-10-147-514-446	Sequence 446, App	780	23	100.0	180	14	US-10-145-087A-470	Sequence 470, App
708	23	100.0	180	14	US-10-147-524-446	Sequence 446, App	781	23	100.0	180	14	US-10-017-889A-470	Sequence 470, App
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710	23	100.0	180	14	US-10-152-394-446	Sequence 446, App	783	23	100.0	180	14	US-10-145-874-446	Sequence 446, App
711	23	100.0	180	14	US-10-152-406-446	Sequence 446, App	784	23	100.0	180	14	US-10-147-497-446	Sequence 446, App
712	23	100.0	180	14	US-10-156-847-446	Sequence 446, App	785	23	100.0	180	14	US-10-152-371-446	Sequence 446, App
713	23	100.0	180	14	US-10-157-778-446	Sequence 446, App	786	23	100.0	180	14	US-10-152-374-446	Sequence 446, App
714	23	100.0	180	14	US-10-157-799-446	Sequence 446, App	787	23	100.0	180	14	US-10-152-375-446	Sequence 446, App
715	23	100.0	180	14	US-10-160-504-446	Sequence 446, App	788	23	100.0	180	14	US-10-152-377-446	Sequence 446, App
716	23	100.0	180	14	US-10-017-191A-470	Sequence 470, App	789	23	100.0	180	14	US-10-152-386-446	Sequence 446, App
717	23	100.0	180	14	US-10-145-634-446	Sequence 446, App	790	23	100.0	180	14	US-10-152-391-446	Sequence 446, App
718	23	100.0	180	14	US-10-147-520-446	Sequence 446, App	791	23	100.0	180	14	US-10-152-399-446	Sequence 446, App
719	23	100.0	180	14	US-10-157-781-446	Sequence 446, App	792	23	100.0	180	14	US-10-156-848-446	Sequence 446, App
720	23	100.0	180	14	US-10-176-989-446	Sequence 446, App	793	23	100.0	180	14	US-10-157-785-446	Sequence 446, App
721	23	100.0	180	14	US-10-366-791-2	Sequence 2, Appli	794	23	100.0	180	14	US-10-157-794-446	Sequence 446, App
722	23	100.0	180	14	US-10-147-491-446	Sequence 446, App	795	23	100.0	180	14	US-10-157-796-446	Sequence 446, App
723	23	100.0	180	14	US-10-152-378-446	Sequence 446, App	796	23	100.0	180	14	US-10-160-500-446	Sequence 446, App
724	23	100.0	180	14	US-10-152-382-446	Sequence 446, App	797	23	100.0	180	14	US-10-164-829A-470	Sequence 470, App
725	23	100.0	180	14	US-10-152-383-446	Sequence 446, App	798	23	100.0	180	14	US-10-164-929A-470	Sequence 470, App
726	23	100.0	180	14	US-10-152-384-446	Sequence 446, App	799	23	100.0	180	14	US-10-121-046-446	Sequence 446, App
727	23	100.0	180	14	US-10-152-387-446	Sequence 446, App	800	23	100.0	180	14	US-10-123-156-446	Sequence 446, App
728	23	100.0	180	14	US-10-152-389-446	Sequence 446, App	801	23	100.0	180	14	US-10-123-214-446	Sequence 446, App
729	23	100.0	180	14	US-10-152-390-446	Sequence 446, App	802	23	100.0	180	14	US-10-125-805-446	Sequence 446, App
730	23	100.0	180	14	US-10-152-392-446	Sequence 446, App	803	23	100.0	180	14	US-10-013-922A-470	Sequence 470, App
731	23	100.0	180	14	US-10-153-756-446	Sequence 446, App	804	23	100.0	180	14	US-10-020-445A-470	Sequence 470, App
732	23	100.0	180	14	US-10-157-784-446	Sequence 446, App	805	23	100.0	180	14	US-10-013-924A-470	Sequence 470, App
733	23	100.0	180	14	US-10-157-797-446	Sequence 446, App	806	23	100.0	180	14	US-10-124-821-446	Sequence 446, App
734	23	100.0	180	14	US-10-158-491-446	Sequence 446, App	807	23	100.0	180	14	US-10-152-385-446	Sequence 446, App
735	23	100.0	180	14	US-10-410-927-2	Sequence 2, Appli	808	23	100.0	180	14	US-10-152-393-446	Sequence 446, App
736	23	100.0	180	14	US-10-143-028A-470	Sequence 470, App	809	23	100.0	180	14	US-10-152-396-446	Sequence 446, App
737	23	100.0	180	14	US-10-143-029A-470	Sequence 470, App	810	23	100.0	180	14	US-10-153-552-446	Sequence 446, App
738	23	100.0	180	14	US-10-142-762-446	Sequence 446, App	811	23	100.0	180	14	US-10-153-840-446	Sequence 446, App
739	23	100.0	180	14	US-10-142-764-446	Sequence 446, App	812	23	100.0	180	14	US-10-156-841-446	Sequence 446, App
740	23	100.0	180	14	US-10-142-766-446	Sequence 446, App	813	23	100.0	180	14	US-10-156-842-446	Sequence 446, App
741	23	100.0	180	14	US-10-145-089A-470	Sequence 470, App	814	23	100.0	180	14	US-10-156-844-446	Sequence 446, App
742	23	100.0	180	14	US-10-145-625-446	Sequence 446, App	815	23	100.0	180	14	US-10-156-845-446	Sequence 446, App
743	23	100.0	180	14	US-10-145-627-446	Sequence 446, App	816	23	100.0	180	14	US-10-156-846-446	Sequence 446, App

817	23	100.0	180	14	US-10-410-552-2	Sequence 2, Appli	890	23	100.0	180	15	US-10-158-784-446	Sequence 446, App
818	23	100.0	180	14	US-10-121-048-446	Sequence 446, App	891	23	100.0	180	15	US-10-158-789-446	Sequence 446, App
819	23	100.0	180	14	US-10-121-052-446	Sequence 446, App	892	23	100.0	180	15	US-10-192-011-446	Sequence 446, App
820	23	100.0	180	14	US-10-121-053-446	Sequence 446, App	893	23	100.0	180	15	US-10-139-963-446	Sequence 446, App
821	23	100.0	180	14	US-10-121-054-446	Sequence 446, App	894	23	100.0	180	15	US-10-140-020-446	Sequence 446, App
822	23	100.0	180	14	US-10-121-063-446	Sequence 446, App	895	23	100.0	180	15	US-10-140-023-446	Sequence 446, App
823	23	100.0	180	14	US-10-123-213-446	Sequence 446, App	896	23	100.0	180	15	US-10-140-809-446	Sequence 446, App
824	23	100.0	180	14	US-10-123-213-446	Sequence 446, App	897	23	100.0	180	15	US-10-140-809-446	Sequence 446, App
825	23	100.0	180	14	US-10-123-291-446	Sequence 446, App	898	23	100.0	180	15	US-10-141-701-446	Sequence 446, App
826	23	100.0	180	14	US-10-123-323-446	Sequence 446, App	899	23	100.0	180	15	US-10-141-754-446	Sequence 446, App
827	23	100.0	180	14	US-10-123-771-446	Sequence 446, App	900	23	100.0	180	15	US-10-141-750-446	Sequence 446, App
828	23	100.0	180	14	US-10-123-911-446	Sequence 446, App	901	23	100.0	180	15	US-10-142-425-446	Sequence 446, App
829	23	100.0	180	14	US-10-123-823-446	Sequence 446, App	902	23	100.0	180	15	US-10-142-430-446	Sequence 446, App
830	23	100.0	180	14	US-10-125-931-446	Sequence 446, App	903	23	100.0	180	15	US-10-143-113-446	Sequence 446, App
831	23	100.0	180	14	US-10-125-932-446	Sequence 446, App	904	23	100.0	180	15	US-10-146-733-446	Sequence 446, App
832	23	100.0	180	15	US-10-125-932-446	Sequence 446, App	905	23	100.0	180	15	US-10-146-732-446	Sequence 446, App
833	23	100.0	180	15	US-10-127-852A-446	Sequence 446, App	906	23	100.0	180	15	US-10-158-731-446	Sequence 446, App
834	23	100.0	180	15	US-10-127-852A-446	Sequence 446, App	907	23	100.0	180	15	US-10-158-731-446	Sequence 446, App
835	23	100.0	180	15	US-10-128-685A-446	Sequence 446, App	908	23	100.0	180	15	US-10-156-843-446	Sequence 446, App
836	23	100.0	180	15	US-10-131-820A-446	Sequence 446, App	909	23	100.0	180	15	US-10-157-786-446	Sequence 446, App
837	23	100.0	180	15	US-10-143-886-446	Sequence 446, App	910	23	100.0	180	15	US-10-157-786-446	Sequence 446, App
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850	23	100.0	180	15	US-10-172-039A-470	Sequence 470, App	923	23	100.0	180	15	US-10-140-927-446	Sequence 446, App
851	23	100.0	180	15	US-10-210-028-470	Sequence 470, App	924	23	100.0	180	15	US-10-147-493-446	Sequence 446, App
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864	23	100.0	180	15	US-10-141-762-446	Sequence 446, App	937	23	100.0	180	16	US-10-437-963-135103	Sequence 135103,
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973 23 100.0 192 16 US-10-343-663A-59 Sequence 59, Appl
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998 23 100.0 201 11 US-09-833-245-1506 Sequence 1506, Ap
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ALIGNMENTS

RESULT 1

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US-10-197-954-120
; Sequence 120, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: Kuster, Hubert
; APPLICANT: Siddiqi, Subaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien
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US-10-197-954-120

Query Match 100.0%; Score 23; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 1 GQPR 4
RESULT 2
US-10-742-344-3
; Sequence 3, Application US/10742344
; Publication No. US20040120918A1
; GENERAL INFORMATION:
; APPLICANT: LINTNER, KARL
; APPLICANT: GABRIELS, DENISE E.
; TITLE OF INVENTION: COSMETIC OR DERMOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: OF CERAMIDES AND POLYPEPTIDES
; FILE REFERENCE: SEDERM 3.0-002
; CURRENT APPLICATION NUMBER: US/10/742,344
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: FR 03 05707
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: see specification as filed for detailed description of lipid
; OTHER INFORMATION: group attachments and preferred embodiments
US-10-742-344-3
Query Match 100.0%; Score 23; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 1 GQPR 4
RESULT 3
US-10-731-921-3
; Sequence 3, Application US/10731921
; Publication No. US20040132667A1
; GENERAL INFORMATION:
; APPLICANT: LINTNER, KARL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING MIXTURES OF TETRAPEPTIDES AND TRIPEPTIDES
; FILE REFERENCE: SEDERM 3.0-001
; CURRENT APPLICATION NUMBER: US/10/731,921
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/FR03/03423
; PRIOR FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: see specification as filed for detailed description of lipid
; OTHER INFORMATION: group attachments and preferred embodiments
US-10-731-921-3
Query Match 100.0%; Score 23; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GQPR 4
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Db 1 GQPR 4

RESULT 4

US-10-760-085-120
; Sequence 120, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K'ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10760,085
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-120

Query Match 100.0%; Score 23; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 1 GQPR 4

RESULT 5

US-09-776-874A-8
; Sequence 8, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09776,874A
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-874A-8

Query Match 100.0%; Score 23; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 6

US-09-988-113-8
; Sequence 8, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-09-988-113-8

Query Match 100.0%; Score 23; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 7

US-10-341-582-8
; Sequence 8, Application US/10341582
; Publication No. US20030161823A1
; GENERAL INFORMATION:
; APPLICANT: Neta Ilan
; APPLICANT: Israel Vlodavsky
; APPLICANT: Oron Yacoby-Zeevi
; APPLICANT: Iris Pecker
; TITLE OF INVENTION: THERAPEUTIC AND COSMETIC USES OF HEPARANASES
; FILE REFERENCE: 25449
; CURRENT APPLICATION NUMBER: US/10/341,582
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-341-582-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 8

US-10-384-451-8
; Sequence 8, Application US/10384451
; Publication No. US20030170860A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25718
; CURRENT FILING DATE: 2003-03-10
; CURRENT APPLICATION NUMBER: US/10/384,451
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-384-451-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 9

US-10-384-450-8
; Sequence 8, Application US/10384450
; Publication No. US20030190737A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25717
; CURRENT APPLICATION NUMBER: US/10/384,450
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
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; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-384-450-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 10

US-10-371-218A-8

; Sequence 8, Application US/10371218A
; Publication No. US20030217375A1
; GENERAL INFORMATION:
; APPLICANT: Zcharia, Eyal
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Metzger, Shula
; APPLICANT: Pecker, Iris
; APPLICANT: Ilan, Neta
; APPLICANT: Chajek-Shaul, Tova
; APPLICANT: Goldshmidt, Orit
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HEPARANASE AND USES THEREOF
; FILE REFERENCE: 25783
; CURRENT APPLICATION NUMBER: US/10/371,218A
; CURRENT FILING DATE: 2003-07-01
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-371-218A-8

Query Match 100.0%; Score 23; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 6 GQPR 9

RESULT 11

US-10-456-573-8
; Sequence 8, Application US/10456573
; Publication No. US20030236215A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25677
; CURRENT APPLICATION NUMBER: US/10/456,573
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 09/435,739
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: US 09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-573-8

Query Match 100.0%; Score 23; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 6 GQPR 9

RESULT 12

US-10-785-116-8

; Sequence 8, Application US/10785116
; Publication No. US2004014247A1
; GENERAL INFORMATION:

; APPLICANT: Becker, Iris
; APPLICANT: Vlodayevsky, Israel
; APPLICANT: Feinstein, Elena

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 27674

; CURRENT APPLICATION NUMBER: US/10/785,116
; CURRENT FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-785-116-8

Query Match 100.0%; Score 23; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 6 GQPR 9

RESULT 13

US-09-920-306-63

; Sequence 63, Application US/09920306
; Publication No. US20040029808A1

; GENERAL INFORMATION:

; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV

; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Hormonal Analyses

; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63
; LENGTH: 12

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide
US-09-920-306-63

Query Match

Best Local Similarity 100.0%; Score 23; DB 11; Length 12;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 5 GQPR 8

RESULT 14

US-09-989-920-263

; Sequence 263, Application US/09989920
; Patent No. US20020172957A1

; GENERAL INFORMATION:

; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve

; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming

; APPLICANT: Liu, Chenghua

; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins

; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920

; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22

; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 263
; LENGTH: 13

; TYPE: PRT
; ORGANISM: Homo sapien

; OTHER INFORMATION: US-09-989-920-263

Query Match

Best Local Similarity 100.0%; Score 23; DB 9; Length 13;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 3 GQPR 6

RESULT 15

US-09-873-637-3

; Sequence 3, Application US/09873637
; Patent No. US20020061543A1

; GENERAL INFORMATION:

; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN

; FILE REFERENCE: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/873,637

; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

; LENGTH: 14
; TYPE: PRT

; ORGANISM: Mus musculus
; OTHER INFORMATION: US-09-873-637-3

Query Match

Best Local Similarity 100.0%; Score 23; DB 9; Length 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 9 GQPR 12

RESULT 16

US-10-327-598-226

; Sequence 226, Application US/10327598
; Publication No. US20040181039A1

; GENERAL INFORMATION:

; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang

; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert

; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: for Making and Using Them

; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 226
; LENGTH: 15

; TYPE: PRT

```
; ORGANISM: canis familiaris;
US-10-327-598-226

Query Match      100.0%; Score 23; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      11 GQPR 14

RESULT 17
US-09-984-017-2
; Sequence 2, Application US/09984017
; Patent No. US20020115614A1
; GENERAL INFORMATION:
; APPLICANT: FRANK, MICHAEL M.
; APPLICANT: JIANG, HAIXIANG J.
; TITLE OF INVENTION: INHIBITION OF COMPLEMENT ACTION
; FILE REFERENCE: 1579-619
; CURRENT APPLICATION NUMBER: US/09/984,017
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US00/10928
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/130,936
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CH2 or CH3 domain of IgG
US-09-984-017-2

Query Match      100.0%; Score 23; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      8 GQPR 11

RESULT 18
US-10-408-765A-3069
; Sequence 3069, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3069
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide containing doubly oxidized tryptophan
; OTHER INFORMATION: (N-formylkynurenine) from the human cardiac
; OTHER INFORMATION: proteome.

; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 2,7_
; OTHER INFORMATION: Xaa = N-formylkynurenine
US-10-408-765A-3069

Query Match      100.0%; Score 23; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      15 GQPR 18

RESULT 19
US-09-843-676-194
; Sequence 194, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-843-676-194

Query Match      100.0%; Score 23; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 20
US-09-438-486-194
; Sequence 194, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-438-486-194

Query Match 100.0%; Score 23; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 21
US-10-053-758-194
; Sequence 194, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-053-758-194

Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 22

US-10-054-295-194
; Sequence 194, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-054-295-194

Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 15 GQPR 18

RESULT 23
US-10-054-611-194
; Sequence 194, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-054-611-194
Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 15 GQPR 18
RESULT 24
US-10-325-810-313
; Sequence 313, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-10-325-810-313

Query Match 100.0%; Score 23; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 25

US-10-877-146-313
Sequence 313, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-10-877-146-313

Query Match 100.0%; Score 23; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 26

US-10-263-162-45
Sequence 45, Application US/10263162
Publication No. US2003018686A1
GENERAL INFORMATION:
APPLICANT: Rosenbaum, et al.
TITLE OF INVENTION: Anti-Angiogenic Peptides

; FILE REFERENCE: REG 810
; CURRENT APPLICATION NUMBER: US/10/263,162
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/326,712
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 22
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-263-162-45

Query Match 100.0%; Score 23; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 8 GQPR 11

RESULT 27
US-10-384-060-15
; Sequence 15, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Honayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide able to nonspecifically activate lymphocytes
US-10-384-060-15

Query Match 100.0%; Score 23; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 7 GQPR 10

RESULT 28
US-09-847-102A-119
; Sequence 119, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Cort, Maribat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leon M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629-00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-119

Query Match 100.0%; Score 23; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 20 GQPR 23

RESULT 29
US-09-820-843A-81
; Sequence 81, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 27
; TYPE: PRT
; ORGANISM: M. tuberculosis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: hypothetical protein Rv1572c
; NAME/KEY: misc feature
; OTHER INFORMATION: gi|2117265
US-09-820-843A-81

Query Match 100.0%; Score 23; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 2 GQPR 5

RESULT 30
US-10-029-386-28116
; Sequence 28116, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: A60MICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28116
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens


```
/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR21 64.0
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.93
/ OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
/ OTHER INFORMATION: SWISSPROT HIT: P21483, EVALUAE 3.90e+00
US-10-029-386-28116

Query Match      100.0%; Score 23; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      28 GQPR 31

RESULT 31
US-10-295-732-2
; Sequence 2, Application US/10295732
; Publication No. US20030104569A1
; GENERAL INFORMATION:
; APPLICANT: Oritani, Kenji
; APPLICANT: Tomiyama, Yoshiaki
; APPLICANT: Matsuzawa, Yuji
; APPLICANT: Kincade, Paul W.
; TITLE OF INVENTION: Proteins Suppressing proliferation of lympho-hematopoietic cells
; FILE REFERENCE: SHIM-003DIV
; CURRENT APPLICATION NUMBER: US/10/295,732
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 09/523,686
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: JP 11/107246
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRP
; ORGANISM: Mus musculus
US-10-295-732-2

Query Match      100.0%; Score 23; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      13 GQPR 16

RESULT 32
US-10-437-963-130130
; Sequence 130130, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

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/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 130130
/ LENGTH: 34
/ TYPE: PRP
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_32320C.1.pep
US-10-437-963-130130

Query Match      100.0%; Score 23; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      1 GQPR 4

RESULT 33
US-10-038-612-70
; Sequence 70, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; FILE REFERENCE: 1242,1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 35
; TYPE: PRP
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: TrkC
US-10-038-612-70

Query Match      100.0%; Score 23; DB 13; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      26 GQPR 29

RESULT 34
US-10-231-417-404
; Sequence 404, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 404
; LENGTH: 35
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-231-417-404

Query Match      100.0%; Score 23; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 GQPR 4
Db      3 GQPR 6

RESULT 35
US-09-104-750-50
; Sequence 50, Application US/09104750
; Publication No. US20030104364A1
; GENERAL INFORMATION:
; APPLICANT: Russell, John
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: Methods and Reagents Useful
; TITLE OF INVENTION: for Detecting Disease of the Breast
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,750
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 6121.US.01
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6121.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030104364A1e
US-09-104-750-50

Query Match      100.0%; Score 23; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      19 GQPR 22

RESULT 36
US-10-437-963-108727
; Sequence 108727, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108727
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_12954C.1.pap
US-10-437-963-108727

Query Match      100.0%; Score 23; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      17 GQPR 20

RESULT 37
US-10-767-701-61720
; Sequence 61720, Application US/10767701
; Publication No. US2004017284A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 61720
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 9850456.pap
US-10-767-701-61720

Query Match      100.0%; Score 23; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      32 GQPR 35

RESULT 38
US-10-012-542-262
; Sequence 262, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
```

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-262

Query Match 100.0%; Score 23; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 16 GQPR 19

RESULT 39
US-10-115-123-262
; Sequence 262, Application US/10115123
; Publication No. US20030065151A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-262

Query Match 100.0%; Score 23; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 16 GQPR 19

RESULT 40
US-09-776-724A-227
; Sequence 227, Application US/09776724A
; Publication No. US20030050455A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: P2011
; CURRENT APPLICATION NUMBER: US/09/776,724A

; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,909
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/669,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,873
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-724A-227

Query Match 100.0%; Score 23; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 35 GQPR 38

RESULT 41
US-10-437-963-152267
; Sequence 152267, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152267
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52335C.1.pep
US-10-437-963-152267

Query Match          100.0%; Score 23; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      6 GQPR 9

RESULT 42
US-10-437-963-151924
; Sequence 151924, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151924
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52022C.1.pep
US-10-437-963-151924

Query Match          100.0%; Score 23; DB 16; Length 40;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      2 GQPR 5

RESULT 43
US-09-864-761-45995
; Sequence 45995, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
```

```
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45995
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008567.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: SWISSPROT HIT: P55067, EVALUATE 8.30e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF125921.1, EVALUATE 8.00e-08
US-09-864-761-45995

Query Match          100.0%; Score 23; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      12 GQPR 15

RESULT 44
US-10-240-145-162
; Sequence 162, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
```

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; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 2000-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 162
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(41)
; OTHER INFORMATION: xaa = X or * as defined in Table 6
US-10-240-145-162

Query Match          100.0%; Score 23; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      29 GQPR 32

RESULT 45
US-10-424-599-145097
; Sequence 145097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145097
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102040C.1.pep
US-10-424-599-145097

Query Match          100.0%; Score 23; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      13 GQPR 16

RESULT 46
US-10-424-599-177895
; Sequence 177895, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177895
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131655C.1.pep
US-10-424-599-177895

Query Match          100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      31 GQPR 34

RESULT 47
US-10-424-599-255629
; Sequence 255629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255629
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72854C.1.pep
US-10-424-599-255629

Query Match          100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      40 GQPR 43

RESULT 48
US-09-864-761-38712
; Sequence 38712, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177895
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(44)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131655C.1.pep
US-10-424-599-177895

Query Match          100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      31 GQPR 34

RESULT 47
US-10-424-599-255629
; Sequence 255629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255629
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72854C.1.pep
US-10-424-599-255629

Query Match          100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
DB      40 GQPR 43

RESULT 48
US-09-864-761-38712
; Sequence 38712, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38712
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022319.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EST_HUMAN HIT: T85631.1, EVALUATE 5.208+00

Query Match 100.0%; Score 23; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 10 GQPR 13

RESULT 49

US-10-437-963-139079
; Sequence 139079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139079
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40406C.1.pap
US-10-437-963-139079

Query Match 100.0%; Score 23; DB 16; Length 46;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 21 GQPR 24

RESULT 50

US-09-864-761-45670
; Sequence 45670, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 45670
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009699.6
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
;; OTHER INFORMATION: SWISSPROT HIT: Q00706, EVALUATE 4.70e+00
;; OTHER INFORMATION: EST_HUMAN HIT: BE777699.1, EVALUATE 1.30e+00
US-09-864-761-45670

Query Match 100.0%; Score 23; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 19 GQPR 22

RESULT 51

US-09-864-761-48301
;; Sequence 48301, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aeomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 48301
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009181.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
;; OTHER INFORMATION: EST_HUMAN HIT: AUI42410.1, EVALUATE 1.00e-11
US-09-864-761-48301

Query Match 100.0%; Score 23; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 11 GQPR 14

RESULT 52

US-09-864-408A-8876
;; Sequence 8876, Application US/09864408A
;; Publication No. US20040009474A1
;; GENERAL INFORMATION:
;; APPLICANT: Leach, Martin D.
;; APPLICANT: Shimkets, Richard A.
;; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encor
;; FILE REFERENCE: 21402-012
;; CURRENT APPLICATION NUMBER: US/09/864,408A
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: 60/206,690
;; PRIOR FILING DATE: 2000-05-24
;; NUMBER OF SEQ ID NOS: 9068
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 8876
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-864-408A-8876

Query Match 100.0%; Score 23; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 20 GQPR 23

RESULT 53

US-10-091-007-26
;; Sequence 26, Application US/10091007
;; Publication No. US20030170782A1
;; GENERAL INFORMATION:
;; APPLICANT: Microbial
;; APPLICANT: Le Page, Richard W F
;; APPLICANT: Hanniffy, Sean B
;; APPLICANT: Wells, Jeremy M

; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-26

Query Match 100.0%; Score 23; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 16 GQPR 19

RESULT 54
US-10-424-599-185208
; Sequence 185208, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185208
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(51)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138257C.1.pap
US-10-424-599-185208

Query Match 100.0%; Score 23; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 17 GQPR 20

RESULT 55
US-10-424-599-180797
; Sequence 180797, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180797
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134274C.1.pap
US-10-424-599-180797

Query Match 100.0%; Score 23; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 56
US-10-424-599-247027
; Sequence 247027, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247027
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65095C.1.pap
US-10-424-599-247027

Query Match 100.0%; Score 23; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 32 GQPR 35

RESULT 57
US-10-424-599-170629
; Sequence 170629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170629
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125093C.1.pap
US-10-424-599-170629


```
Query Match      100.0%; Score 23; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
        ||||
DB      16 GQPR 19

RESULT 58
US-10-424-599-151840
; Sequence 151840, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151840
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108135C.1.pep
US-10-424-599-151840

Query Match      100.0%; Score 23; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
        ||||
DB      14 GQPR 17

RESULT 59
US-10-029-386-34129
; Sequence 34129, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34129
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004624.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.46
; OTHER INFORMATION: SWISSPROT HIT: Q04781, EVALU8 8.10e+00
US-10-029-386-34129

Query Match      100.0%; Score 23; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
        ||||
DB      2 GQPR 5
```

```
RESULT 60
US-10-437-963-155414
; Sequence 155414, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 155414
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5517C.1.pep
US-10-437-963-155414

Query Match      100.0%; Score 23; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
        ||||
DB      16 GQPR 19

RESULT 61
US-09-864-408A-6778
; Sequence 6778, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6778
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-6778

Query Match      100.0%; Score 23; DB 11; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
        ||||
DB      8 GQPR 11

RESULT 62
US-10-424-599-181996
; Sequence 181996, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 181996
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135356C.1.pep
US-10-424-599-181996

Query Match      100.0%; Score 23; DB 15; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      1 GQPR 4

RESULT 63
US-10-424-599-145320
; Sequence 145320, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145320
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102243C.1.pep
US-10-424-599-145320

Query Match      100.0%; Score 23; DB 15; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      10 GQPR 13

RESULT 64
US-10-424-599-155931
; Sequence 155931, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
```

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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155931
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111826C.1.pep
US-10-424-599-155931

Query Match      100.0%; Score 23; DB 15; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      35 GQPR 38

RESULT 65
US-09-864-408A-5620
; Sequence 5620, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5620
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5620

Query Match      100.0%; Score 23; DB 11; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      21 GQPR 24

RESULT 66
US-10-424-599-177632
; Sequence 177632, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177632
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131417C.1.pep
US-10-424-599-177632

Query Match      100.0%; Score 23; DB 15; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 27 GQPR 30

RESULT 67

US-10-424-599-233719
; Sequence 233719, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 233719

; LENGTH: 63

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_53073C.1.pap

US-10-424-599-233719

Query Match

Best Local Similarity 100.0%; Score 23; DB 15; Length 63;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 36 GQPR 39

RESULT 68

US-10-437-963-163011
; Sequence 163011, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 163011

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_62046C.1.pap

US-10-437-963-163011

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 64;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 2 GQPR 5

RESULT 69

US-10-437-963-155904
; Sequence 155904, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 155904

; LENGTH: 65

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_55623C.1.pap

US-10-437-963-155904

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 24 GQPR 27

RESULT 70

US-10-437-963-104594
; Sequence 104594, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 104594

; LENGTH: 67

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_101913C.1.pap

US-10-437-963-104594

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 67;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 28 GQPR 31

RESULT 71

US-09-864-408A-6184
; Sequence 6184, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encoded by
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6184
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-6184

Query Match 100.0%; Score 23; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 45 GQPR 48

RESULT 72

US-10-105-004-139
; Sequence 139, Application US/10105004
; Publication No. US20030105002A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Jeffrey
; Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/105,004
; FILING DATE: 22-Mar-2002
; APPLICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,477
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-022.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 139:

US-10-105-004-139

Query Match 100.0%; Score 23; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 42 GQPR 45

RESULT 73

US-10-437-963-106825
; Sequence 106825, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106825
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT4530_11234C.1.pap
US-10-437-963-106825

Query Match 100.0%; Score 23; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 55 GQPR 58

RESULT 74

US-10-424-599-143493
; Sequence 143493, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143493
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(70)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_100589C.1.pap
US-10-424-599-143493

Query Match 100.0%; Score 23; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
DB 43 GQPR 46

RESULT 75
US-10-424-599-211412
; Sequence 211412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 211412
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32931C.1.pep
US-10-424-599-211412

Query Match 100.0%; Score 23; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
DB 53 GQPR 56

Search completed: May 17, 2005, 10:10:47
Job time : 148 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 09:58:31 ; Search time 169 Seconds
(without alignments)
9.154 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq19808:*

2: Geneseq19908:*

3: Geneseq20008:*

4: Geneseq20018:*

5: Geneseq20028:*

6: Geneseq20038:*

7: Geneseq20038:*

8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	4	3	AAB07766
2	23	100.0	4	4	AAB92377
3	23	100.0	4	7	ADJ81639
4	23	100.0	4	8	ADN03394
5	23	100.0	4	8	ADQ93809
6	23	100.0	4	8	ADR03553
7	23	100.0	4	8	ADR42229
8	23	100.0	9	2	AAV02344
9	23	100.0	9	3	AAB08848
10	23	100.0	9	7	ADG88798
11	23	100.0	9	8	ADL16377
12	23	100.0	9	8	ADM48714
13	23	100.0	10	2	AAV34181
14	23	100.0	10	2	AAV17071
15	23	100.0	11	1	AAP60496
16	23	100.0	11	6	ABU03391
17	23	100.0	11	7	ADD23535
18	23	100.0	12	5	AAU87007
19	23	100.0	13	1	AAP51019
20	23	100.0	13	5	ABU60996
21	23	100.0	14	4	AAW98739
22	23	100.0	15	1	AAW82447
23	23	100.0	15	2	AAV13277
24	23	100.0	15	2	AAV13300
25	23	100.0	15	2	AAV13251

26	23	100.0	15	7	ADM08091	Adm08091	Canine im
27	23	100.0	15	7	ADM07959	Adm07959	Canine im
28	23	100.0	16	6	ABP55617	Abp55617	Human cyt
29	23	100.0	17	3	AAB36861	Aab36861	Residue
30	23	100.0	18	2	AAR49648	Aar49648	Sequence
31	23	100.0	18	2	AAR49647	Aar49647	Sequence
32	23	100.0	18	2	AAR49646	Aar49646	Sequence
33	23	100.0	18	2	AAR49534	Aar49534	Human Ig
34	23	100.0	18	2	AAR49533	Aar49533	Human Ig
35	23	100.0	18	2	AAR49532	Aar49532	Human Ig
36	23	100.0	22	6	ABR57545	Abr57545	Anti-angi
37	23	100.0	23	1	AAP30407	Aap30407	Sequence
38	23	100.0	23	1	AAP30405	Aap30405	Sequence
39	23	100.0	23	1	AAP30404	Aap30404	Sequence
40	23	100.0	23	1	AAP30406	Aap30406	Sequence
41	23	100.0	23	1	AAP30409	Aap30409	Sequence
42	23	100.0	23	8	ADH89371	Adh89371	Human tra
43	23	100.0	23	8	ADS97551	Ads97551	Dementia
44	23	100.0	24	1	AAP30413	Aap30413	Sequence
45	23	100.0	25	5	AAU89298	Aau89298	Insulin/i
46	23	100.0	27	7	ABO23580	Abo23580	Mycobacte
47	23	100.0	28	2	AAW37936	Aaw37936	Herpes vi
48	23	100.0	28	3	AAV56879	Aay56879	Peptide i
49	23	100.0	31	8	ABO54482	Abo54482	Human gen
50	23	100.0	33	4	ABO51356	Abo51356	Mouse blo
51	23	100.0	35	2	AAV19644	Aay19644	SEQ ID NO
52	23	100.0	35	3	AAV98355	Aay98355	Alpha D p
53	23	100.0	35	4	AAW82815	Aaw82815	Human imm
54	23	100.0	35	5	AAU83474	Aau83474	Human pho
55	23	100.0	36	7	ABW00600	Abw00600	BS136 epi
56	23	100.0	37	3	AAV86343	Aay86343	Human gen
57	23	100.0	37	6	ABO53488	Abo53488	Novel hum
58	23	100.0	38	7	ABO23432	Abo23432	Amino aci
59	23	100.0	38	8	ADR20820	Adr20820	Human sec
60	23	100.0	39	2	AAW25684	Aar25684	Exon VII
61	23	100.0	40	8	ADP45479	Adp45479	Human col
62	23	100.0	41	4	AAU68589	Aau68589	Human nov
63	23	100.0	41	4	AAW37357	Aam37357	Peptide #
64	23	100.0	41	4	AAW91448	Aam91448	Human imm
65	23	100.0	41	4	AAW64399	Aam64399	Human bra
66	23	100.0	41	4	ABG58845	Abg58845	Human liv
67	23	100.0	42	5	ABG80821	Abg80821	Rat SP-A
68	23	100.0	42	8	ADG97549	Adg97549	Dementia
69	23	100.0	43	2	AAW95499	Aar95499	E85, mono
70	23	100.0	43	4	ABG26421	Abg26421	Novel hum
71	23	100.0	43	5	AAW21238	Aae21238	Human gen
72	23	100.0	43	7	ADI21604	Adi21604	Novel hum
73	23	100.0	44	4	AAW89537	Adi21603	Novel hum
74	23	100.0	44	4	AAO03183	Aao03183	Human pol
75	23	100.0	46	4	AAW19030	Aam19030	Peptide #
76	23	100.0	46	4	ABW38236	Abw38236	Peptide #
77	23	100.0	46	4	AAW31669	Aam31669	Peptide #
78	23	100.0	46	4	ABW23414	Abw23414	Protein #
79	23	100.0	46	4	AAW71387	Aam71387	Human bon
80	23	100.0	46	4	AAW58864	Aam58864	Human bon
81	23	100.0	46	4	ABG53089	Abg53089	Human liv
82	23	100.0	46	5	ABG41188	Abg41188	Human pep
83	23	100.0	47	2	AAW95034	Aar95034	Fragment
84	23	100.0	49	4	ABU01054	Aau01054	Human sec
85	23	100.0	49	4	ABW42912	Abw42912	Peptide #
86	23	100.0	49	4	AAW36732	Aam36732	Peptide #
87	23	100.0	49	4	AAW37627	Aam37627	Human bon
88	23	100.0	49	4	AAW63813	Aam63813	Human bra
89	23	100.0	49	4	ABG58321	Abg58321	Human liv
90	23	100.0	49	5	ABG45854	Abg45854	Human pep
91	23	100.0	50	4	AAW38222	Aam38222	Peptide #
92	23	100.0	50	4	AAW78006	Aam78006	Human bon
93	23	100.0	50	4	AAW39742	Aau39742	Propionib
94	23	100.0	50	5	ABG47019	Abg47019	Human pep
95	23	100.0	50	5	ABF35465	Abp35465	Human ORF
96	23	100.0	50	5	AAW50385	Aam50385	Mouse hep
97	23	100.0	50	5	ADR41540	Adr41540	Human CD-

99	23	100.0	50	6	ABM36261	Abm36261 Propionib	172	23	100.0	68	4	AAU54837	Aau54837 Propionib
100	23	100.0	51	4	AAU53376	Aau53376 Propionib	173	23	100.0	68	5	ABP34119	Abp34119 Human ORF
101	23	100.0	51	4	AAU51468	Aau51468 Propionib	174	23	100.0	68	6	ABM51356	Abm51356 Propionib
102	23	100.0	51	4	AAU51512	Aau51512 Propionib	175	23	100.0	68	7	ABO07413	Abm07413 Human RIE
103	23	100.0	51	4	AAU64415	Aau64415 Propionib	176	23	100.0	68	7	ADH83479	Adh83479 RGD/Solur
104	23	100.0	51	4	AAU03613	Aau03613 Group B S	177	23	100.0	68	8	ADK01862	Adk01862 Hepatitis
105	23	100.0	51	5	ABP04226	Abp04226 Human ORF	178	23	100.0	69	4	ABB70463	Abb70463 Drosophil
106	23	100.0	51	6	ABM60934	Abm60934 Propionib	179	23	100.0	69	4	AU55004	Au55004 Propionib
107	23	100.0	51	6	ABM47987	Abm47987 Propionib	180	23	100.0	69	5	ABP06441	Abp06441 Human ORF
108	23	100.0	51	6	ABM51895	Abm51895 Propionib	181	23	100.0	69	5	ADK34226	Adk34226 Novel hum
109	23	100.0	51	6	ABM48031	Abm48031 Propionib	182	23	100.0	69	6	ABM51523	Abm51523 Propionib
110	23	100.0	53	4	AAU68680	Aau68680 Human imm	183	23	100.0	70	4	AU50626	Au50626 Propionib
111	23	100.0	53	7	ADH62382	Adh62382 Rhizomuc	184	23	100.0	70	6	ABM47145	Abm47145 Propionib
112	23	100.0	54	4	AAU55625	Aau55625 Propionib	185	23	100.0	71	4	AAU94044	Aau94044 Human rep
113	23	100.0	54	6	ABM52144	Abm52144 Propionib	186	23	100.0	71	4	AU55545	Au55545 Propionib
114	23	100.0	55	4	AAU50648	Aau50648 Propionib	187	23	100.0	71	6	ABM52064	Abm52064 Propionib
115	23	100.0	55	4	AAU58126	Aau58126 Propionib	188	23	100.0	72	4	AAU41006	Aau41006 Propionib
116	23	100.0	55	4	AAU40074	Aau40074 Propionib	189	23	100.0	72	4	AAU31079	Aau31079 Novel hum
117	23	100.0	55	6	ABM36593	Abm36593 Propionib	190	23	100.0	72	6	ABM37525	Abm37525 Propionib
118	23	100.0	55	6	ABM47167	Abm47167 Propionib	191	23	100.0	72	8	ABO58681	Abm58681 Human gen
119	23	100.0	55	6	ABM46445	Abm46445 Propionib	192	23	100.0	73	4	AU62030	Au62030 Propionib
120	23	100.0	55	8	ABO60495	Abm60495 Human gen	193	23	100.0	73	4	ABG1663	Abg1663 Propionib
121	23	100.0	56	4	AAU41744	Aau41744 Propionib	194	23	100.0	73	4	ABG17830	Abg17830 Novel hum
122	23	100.0	56	6	ABM38263	Abm38263 Propionib	195	23	100.0	73	6	ABM58182	Abm58182 Propionib
123	23	100.0	57	4	AAO02186	Aao02186 Human pol	196	23	100.0	73	6	ABM58549	Abm58549 Propionib
124	23	100.0	57	4	AAU42779	Aau42779 Propionib	197	23	100.0	74	2	AAU02663	Aau02663 Human sec
125	23	100.0	57	4	AAU44783	Aau44783 Propionib	198	23	100.0	74	4	ABM87383	Abm87383 Human gen
126	23	100.0	57	4	AAU65234	Aau65234 Propionib	199	23	100.0	74	4	AAU82713	Aau82713 Human imm
127	23	100.0	57	6	ABM39298	Abm39298 Propionib	200	23	100.0	74	4	AU52503	Au52503 Propionib
128	23	100.0	57	6	ABM61753	Abm61753 Propionib	201	23	100.0	74	4	AU55521	Au55521 Propionib
129	23	100.0	57	6	ABM41302	Abm41302 Propionib	202	23	100.0	74	5	ABG65379	Abg65379 Human alb
130	23	100.0	58	4	ABM67240	Abm67240 Propionib	203	23	100.0	74	6	ABM52040	Abm52040 Propionib
131	23	100.0	58	4	AAU53389	Aau53389 Propionib	204	23	100.0	74	6	ABM49022	Abm49022 Propionib
132	23	100.0	58	5	ABP09132	Abp09132 Human ORF	205	23	100.0	74	7	ADA07342	Ada07342 Human sec
133	23	100.0	58	5	ABP34416	Abp34416 Human ORF	206	23	100.0	74	8	ADL78646	Adl78646 Albumin f
134	23	100.0	58	6	ABU09599	Abu09599 Human cyt	207	23	100.0	74	8	ADN41084	Adn41084 Novel hum
135	23	100.0	58	6	ABM49908	Abm49908 Propionib	208	23	100.0	74	8	ABO55223	Abm55223 Human gen
136	23	100.0	58	6	ABM63759	Abm63759 Propionib	209	23	100.0	75	7	ADL72462	Adl72462 Human end
137	23	100.0	59	4	AAU56513	Aau56513 Propionib	210	23	100.0	75	7	AAU42470	Aau42470 Propionib
138	23	100.0	59	4	AAU39984	Aau39984 Propionib	211	23	100.0	76	6	ABM38989	Abm38989 Propionib
139	23	100.0	59	6	ABM33032	Abm33032 Propionib	212	23	100.0	77	4	AU53862	Au53862 Propionib
140	23	100.0	59	6	ABM36503	Abm36503 Propionib	213	23	100.0	77	5	ABP34427	Abp34427 Human ORF
141	23	100.0	59	8	ADL97548	Adl97548 Dementia	214	23	100.0	77	6	ABM50381	Abm50381 Propionib
142	23	100.0	60	2	AAU60318	Aau60318 Human end	215	23	100.0	78	3	AGL19072	Agl19072 Zea may
143	23	100.0	60	4	AAU90064	Aau90064 Human imm	216	23	100.0	78	4	AU53653	Au53653 Propionib
144	23	100.0	60	4	AAU83999	Aau83999 Human imm	217	23	100.0	78	4	AAU41173	Aau41173 Propionib
145	23	100.0	60	4	AAU51911	Aau51911 Propionib	218	23	100.0	78	4	AAU30416	Aau30416 Novel hum
146	23	100.0	60	6	ABM48430	Abm48430 Propionib	219	23	100.0	78	6	ABM50172	Abm50172 Propionib
147	23	100.0	60	6	ABM64761	Abm64761 Propionib	220	23	100.0	78	6	ABM37692	Abm37692 Propionib
148	23	100.0	60	7	ABO61526	Abm61526 Klebsiell	221	23	100.0	79	4	AU58510	Au58510 Propionib
149	23	100.0	61	8	ADG22289	Adg22289 Cyanophag	222	23	100.0	79	6	ABM55029	Abm55029 Propionib
150	23	100.0	62	4	AAU46690	Aau46690 Propionib	223	23	100.0	80	4	AAU62784	Aau62784 Propionib
151	23	100.0	62	4	AAU51796	Aau51796 Propionib	224	23	100.0	80	4	ABM15979	Abm15979 Human ner
152	23	100.0	62	4	AAU06281	Aau06281 Human foe	225	23	100.0	80	6	ABM59303	Abm59303 Propionib
153	23	100.0	62	5	ABP33837	Abp33837 Human ORF	226	23	100.0	81	4	ABM50101	Abm50101 Human bra
154	23	100.0	62	6	ABU10042	Abu10042 Human cyt	227	23	100.0	81	4	ABG01739	Abg01739 Novel hum
155	23	100.0	62	6	ABM48315	Abm48315 Propionib	228	23	100.0	82	4	AAU71270	Aau71270 Human gen
156	23	100.0	62	6	ABM43209	Abm43209 Propionib	229	23	100.0	82	4	AAU78973	Aau78973 Human pro
157	23	100.0	62	6	ABM65776	Abm65776 Propionib	230	23	100.0	82	4	AU53683	Au53683 Propionib
158	23	100.0	63	4	AAU44071	Aau44071 Propionib	231	23	100.0	82	4	AU63785	Au63785 Propionib
159	23	100.0	63	6	ABU09600	Abu09600 Human cyt	232	23	100.0	82	4	AAU43502	Aau43502 Propionib
160	23	100.0	63	6	ABM40590	Abm40590 Propionib	233	23	100.0	82	4	ABG05988	Abg05988 Novel hum
161	23	100.0	64	4	ABG08148	Abg08148 Novel hum	234	23	100.0	82	5	ABM83796	Abm83796 Human cal
162	23	100.0	65	4	AAU47579	Aau47579 Propionib	235	23	100.0	82	5	ABG63449	Abg63449 Human alb
163	23	100.0	65	6	ABM44098	Abm44098 Propionib	236	23	100.0	82	6	ADA57560	Ada57560 Human sec
164	23	100.0	67	4	AAU67187	Aau67187 Propionib	237	23	100.0	82	6	ABM60304	Abm60304 Propionib
165	23	100.0	67	4	AAU64827	Aau64827 Propionib	238	23	100.0	82	6	ABM50202	Abm50202 Propionib
166	23	100.0	67	4	AAU43201	Aau43201 Propionib	239	23	100.0	82	6	ABM40021	Abm40021 Propionib
167	23	100.0	67	4	ABM17351	Abm17351 Human ner	240	23	100.0	82	6	ADA41454	Ada41454 Human sec
168	23	100.0	67	5	ABP04739	Abp04739 Human ORF	241	23	100.0	82	7	ADC74575	Adc74575 Human sec
169	23	100.0	67	6	ABM63706	Abm63706 Propionib	242	23	100.0	82	8	ADL76714	Adl76714 Albumin f
170	23	100.0	67	6	ABM61346	Abm61346 Propionib	243	23	100.0	82	8	ABO55288	Abm55288 Human gen
171	23	100.0	67	6	ABM39720	Abm39720 Propionib	244	23	100.0	83	3	AAG41117	Aag41117 Zea may

245	23	100.0	83	4	AAM95977	Aam95977 Human rep	318	23	100.0	107	2	AAR67439	Aar67439 OKT3 mono
246	23	100.0	83	4	ABG96508	Abb96508 Human tes	319	23	100.0	107	3	AGG22650	Agg22650 Zea may
247	23	100.0	84	3	ABG35192	Agg35192 Zea may	320	23	100.0	107	4	AU40683	Aau40683 Propionib
248	23	100.0	85	7	ADN11806	Adn11806 c-Fps SH2	321	23	100.0	107	5	ABP41236	Abp41236 Human ova
249	23	100.0	86	4	AM92636	Aam92636 Human dig	322	23	100.0	107	6	ABM37202	Abm37202 Propionib
250	23	100.0	86	4	AAU52558	Aau52558 Propionib	323	23	100.0	107	7	ADD25814	Add25814 Binding d
251	23	100.0	86	4	AAU22630	Aau22630 Novel hum	324	23	100.0	107	7	ADD25815	Add25815 Binding d
252	23	100.0	86	5	ABP11210	Abp11210 Human ORF	325	23	100.0	107	7	ADD25816	Add25816 Binding d
253	23	100.0	86	6	AM49077	Abm49077 Propionib	326	23	100.0	107	7	ADD25818	Add25818 Binding d
254	23	100.0	86	7	ADB32470	Adb32470 Human nov	327	23	100.0	107	7	ADD25817	Add25817 Binding d
255	23	100.0	87	4	AU17569	Aau17569 Novel sig	328	23	100.0	107	7	ADD25661	Add25661 Binding d
256	23	100.0	87	4	AM89444	Aam89444 Human imm	329	23	100.0	107	8	ADF89744	Adf89744 Human Clo
257	23	100.0	87	4	AAO9077	Aao9077 Human pol	330	23	100.0	107	8	ADH75386	Adh75386 Human Igg
258	23	100.0	87	4	AU43833	Aau43833 Propionib	331	23	100.0	107	8	ADJ52133	Adj52133 CH1 delet
259	23	100.0	87	4	AU87465	Aau87465 Novel cen	332	23	100.0	107	8	ADJ52130	Adj52130 CH1 delet
260	23	100.0	87	5	ABP64189	Abp64189 Human ORF	333	23	100.0	107	8	ADL90102	Adl90102 Human imm
261	23	100.0	87	6	ABM40352	Abm40352 Propionib	334	23	100.0	107	8	ADN36891	Adn36891 CH3 regio
262	23	100.0	87	7	ADB94277	Adb94277 Human nov	335	23	100.0	107	8	ADO60485	Ado60485 Humanised
263	23	100.0	87	8	ADI54780	Adi54780 Novel hum	336	23	100.0	107	8	ADS84435	Ads84435 Human ant
264	23	100.0	88	4	ABB36172	Abb36172 Peptide #	337	23	100.0	107	8	ADR68577	Adr68577 Human ant
265	23	100.0	88	4	AM29663	Aam29663 Peptide #	338	23	100.0	108	3	AB42554	Ab42554 Human ORF
266	23	100.0	88	4	ABB21553	Abb21553 Protein #	339	23	100.0	108	4	AM21575	Aam21575 Peptide #
267	23	100.0	88	4	ABG51016	Abg51016 Human liv	340	23	100.0	108	4	ABB43928	Abb43928 Peptide #
268	23	100.0	88	4	AM04865	Aam04865 Peptide #	341	23	100.0	108	4	AM37854	Aam37854 Peptide #
269	23	100.0	88	5	ABG38958	Abg38958 Human pep	342	23	100.0	108	4	ABB26843	Abb26843 Protein #
270	23	100.0	89	4	AM92655	Aam92655 Human dig	343	23	100.0	108	4	AM77654	Aam77654 Human bon
271	23	100.0	89	4	AM60091	Aam60091 Human tra	344	23	100.0	108	4	AM64918	Aam64918 Human bra
272	23	100.0	89	4	ABB16016	Abb16016 Human ner	345	23	100.0	108	4	ABG59302	Abg59302 Human liv
273	23	100.0	89	4	AAU22649	Aau22649 Novel hum	346	23	100.0	108	5	ABG46686	Abg46686 Human pep
274	23	100.0	89	7	ADB32489	Adb32489 Human nov	347	23	100.0	108	5	AAE28090	Aae28090 Human imm
275	23	100.0	89	7	ADJ68974	Adj68974 Human hea	348	23	100.0	109	4	AM89355	Aam89355 Human imm
276	23	100.0	89	7	ADJ68975	Adj68975 Human hea	349	23	100.0	109	4	ABG01586	Abg01586 Novel hum
277	23	100.0	91	4	AAU60396	Aau60396 Propionib	350	23	100.0	110	4	AAU62185	Aau62185 Propionib
278	23	100.0	91	6	AM56915	Aam56915 Propionib	351	23	100.0	110	4	AAU40774	Aau40774 Propionib
279	23	100.0	91	7	ADH76885	Adh76885 Mouse SOX	352	23	100.0	110	6	ABM37293	Abm37293 Propionib
280	23	100.0	92	3	AB41836	Aab41836 Human COL	353	23	100.0	110	6	ABM58704	Abm58704 Propionib
281	23	100.0	92	4	AAU77595	Aau77595 Human col	354	23	100.0	110	8	ABO56225	Ab056225 Human gen
282	23	100.0	92	8	AM80295	Aam80295 Tumour-as	355	23	100.0	110	8	ADR59167	Adr59167 Human Igg
283	23	100.0	94	4	AAU50673	Aau50673 Propionib	356	23	100.0	111	2	AAW13461	Aaw13461 Headpiece
284	23	100.0	94	4	ABG17384	Abg17384 Novel hum	357	23	100.0	111	4	AM88837	Aam88837 Human imm
285	23	100.0	94	5	ABP41413	Abp41413 Human ova	358	23	100.0	111	4	AAO02130	Aao02130 Human pol
286	23	100.0	94	6	ABM47192	Abm47192 Propionib	359	23	100.0	111	8	ADM87720	Adm87720 Human EST
287	23	100.0	95	4	ABG28613	Abg28613 Novel hum	360	23	100.0	112	3	AAW13459	Aaw13459 Headpiece
288	23	100.0	95	5	ADK35495	Adk35495 Novel hum	361	23	100.0	112	3	AAW13459	Aaw13459 Headpiece
289	23	100.0	95	7	ABO67894	Ab067894 Pseudomon	362	23	100.0	112	4	AAU43924	Aau43924 Propionib
290	23	100.0	96	4	AAO02842	Aao02842 Human pol	363	23	100.0	112	6	ABM40443	Abm40443 Propionib
291	23	100.0	96	6	ABO00435	Ab000435 Novel hum	364	23	100.0	112	8	ADR59166	Adr59166 Optimum C
292	23	100.0	96	6	ADB17005	Adb17005 Propionib	365	23	100.0	113	7	ABJ38539	Abj38539 Human son
293	23	100.0	98	4	AAU58604	Aau58604 Propionib	366	23	100.0	113	7	ABO63581	Ab063581 Klebssteli
294	23	100.0	98	4	ABG22290	Abg22290 Novel hum	367	23	100.0	113	8	ABO57697	Ab057697 Human gen
295	23	100.0	98	6	ABM55123	Abm55123 Propionib	368	23	100.0	114	4	AM38036	Aam38036 Peptide #
296	23	100.0	99	4	AAU52200	Aau52200 Propionib	369	23	100.0	114	4	ABB26980	Abb26980 Protein #
297	23	100.0	99	6	ABM48719	Abm48719 Propionib	370	23	100.0	114	4	AM77817	Aam77817 Human bon
298	23	100.0	100	4	ABM11942	Abm11942 Human dia	371	23	100.0	114	4	ABG59471	Abg59471 Human liv
299	23	100.0	100	4	AM79957	Aam79957 Human pro	372	23	100.0	114	5	ABG46848	Abg46848 Human pep
300	23	100.0	100	4	ABG93289	Aab93289 Human pro	373	23	100.0	115	4	AAU47966	Aau47966 Human col
301	23	100.0	100	8	ADF89743	Adf89743 Human Clo	374	23	100.0	115	6	ADA55196	Ada55196 Human pro
302	23	100.0	101	5	ADP08907	Adp08907 Human ORF	375	23	100.0	115	8	ADR09355	Adr09355 Human pro
303	23	100.0	102	3	AAU32715	Aau32715 Zea may	376	23	100.0	116	4	AAU49757	Aau49757 Propionib
304	23	100.0	102	4	AAU56849	Aau56849 Propionib	377	23	100.0	116	5	ABP07764	Abp07764 Human ORF
305	23	100.0	102	4	AAU99228	Aau99228 Human pro	378	23	100.0	116	6	ABM46276	Abm46276 Propionib
306	23	100.0	102	5	ABP03349	Abp03349 Human ORF	379	23	100.0	117	3	AAW36147	Aaw36147 Rat eosin
307	23	100.0	102	6	ABM53368	Abm53368 Propionib	380	23	100.0	117	3	AAW44109	Aaw44109 Human can
308	23	100.0	102	7	ADB65769	Adb65769 Human pro	381	23	100.0	117	4	AM88573	Aam88573 Human imm
309	23	100.0	104	2	AAU12501	Aau12501 Human 5'	382	23	100.0	117	4	AAO03150	Aao03150 Human pol
310	23	100.0	104	3	AAU12424	Aau12424 Zea may	383	23	100.0	118	3	AB45071	Ab45071 Human sec
311	23	100.0	105	4	AM84107	Aam84107 Human imm	384	23	100.0	118	4	AM78637	Aam78637 Human pro
312	23	100.0	105	4	AAO00397	Aao00397 Human pol	385	23	100.0	118	4	AAO12123	Aao12123 Human pol
313	23	100.0	106	3	AAU32314	Aau32314 Rice neut	386	23	100.0	118	4	ABG22738	Abg22738 Novel hum
314	23	100.0	107	2	AAU27681	Aau27681 Human imm	387	23	100.0	119	4	AM87975	Aam87975 Human imm
315	23	100.0	107	2	AAU41718	Aau41718 Undefined	388	23	100.0	119	4	AAO03225	Aao03225 Human pol
316	23	100.0	107	2	AAU41685	Aau41685 Undefined	389	23	100.0	119	4	AAU42649	Aau42649 Propionib
317	23	100.0	107	2	AAU41714	Aau41714 Undefined	390	23	100.0	119	6	ABM39168	Abm39168 Propionib

391	23	100.0	120	3	AAG16111	Aag16111 Arabidops	464	23	100.0	136	6	ABP75637	Abp75637 Human sec
392	23	100.0	120	7	ADM04825	Adm04825 Human pro	465	23	100.0	136	8	ADG22372	Adg22372 Cyanophag
393	23	100.0	121	4	RAU65294	Rau65294 Propionib	466	23	100.0	137	3	RAG33352	Rag33352 Zea may
394	23	100.0	121	4	AAU61612	Aau61612 Propionib	467	23	100.0	137	3	AGG07099	Agg07099 Arabidops
395	23	100.0	121	6	ABM61813	Abm61813 Propionib	468	23	100.0	137	3	AGG47461	Agg47461 Arabidops
396	23	100.0	121	6	ABM58131	Abm58131 Propionib	469	23	100.0	138	3	AY70578	Ay70578 Salmonell
397	23	100.0	123	3	AAB53621	Aab53621 Human col	470	23	100.0	138	4	ABG25309	Abg25309 Novel hum
398	23	100.0	123	4	AAO00225	Aao00225 Human pol	471	23	100.0	139	3	ABA42106	Aba42106 Human ORF
399	23	100.0	123	4	AAU41835	Aau41835 Propionib	472	23	100.0	139	5	ABP58510	Abp58510 Human mat
400	23	100.0	123	4	ABG00522	Abg00522 Novel hum	473	23	100.0	139	5	ABP58510	Abp58510 Human mat
401	23	100.0	123	6	ABM38354	Abm38354 Propionib	474	23	100.0	139	7	ADJ70416	Adj70416 Human pol
402	23	100.0	124	4	AAO43325	Aao43325 Human pol	475	23	100.0	140	4	AAO02927	Aao02927 Human sec
403	23	100.0	124	4	ABG02519	Abg02519 Novel hum	476	23	100.0	141	2	AAO27815	Aao27815 Human sec
404	23	100.0	124	4	ABG16821	Abg16821 Novel hum	477	23	100.0	141	3	AAV32316	Aav32316 Soybean n
405	23	100.0	124	7	ADF60304	Adf60304 Human con	478	23	100.0	141	4	AAV32316	Aav32316 Soybean n
406	23	100.0	124	7	ADF06217	Adf06217 Bacterial	479	23	100.0	141	4	ABM18786	Abm18786 Peptide #
407	23	100.0	125	4	AAU41925	Aau41925 Propionib	480	23	100.0	141	4	ABM18786	Abm18786 Peptide #
408	23	100.0	125	6	ABM38444	Abm38444 Propionib	481	23	100.0	141	4	AAV32316	Aav32316 Soybean n
409	23	100.0	126	2	AAW97351	Aaw97351 Amino aci	482	23	100.0	141	4	ABM32145	Abm32145 Protein #
410	23	100.0	126	3	AAV32317	Aav32317 Wheat neu	483	23	100.0	141	4	AAW1016	Aaw1016 Human bon
411	23	100.0	126	3	AAV32317	Aav32317 Wheat neu	484	23	100.0	141	4	AAW1016	Aaw1016 Human bon
412	23	100.0	127	6	ADA57554	Ada57554 Human sec	485	23	100.0	141	4	AAW1016	Aaw1016 Human bon
413	23	100.0	127	6	ADA41446	Ada41446 Human sec	486	23	100.0	141	4	AAW1016	Aaw1016 Human bon
414	23	100.0	127	7	ADC74566	Adc74566 Human sec	487	23	100.0	141	6	ABO14308	Abol14308 Novel hum
415	23	100.0	127	7	ADC74566	Adc74566 Human sec	488	23	100.0	141	7	ABO70522	Abol70522 Pseudomon
416	23	100.0	127	7	ADF94884	Adf94884 Human gen	489	23	100.0	141	8	ADG78716	Adg78716 Human sec
417	23	100.0	127	8	ADN41129	Adn41129 Novel hum	490	23	100.0	141	8	ADG78716	Adg78716 Human sec
418	23	100.0	128	2	AAO2690	Aao2690 Human sec	491	23	100.0	141	8	ADG78716	Adg78716 Human sec
419	23	100.0	128	4	AAO00602	Aao00602 Human pol	492	23	100.0	141	8	ADG78716	Adg78716 Human sec
420	23	100.0	128	4	AAU41509	Aau41509 Propionib	493	23	100.0	142	4	ADG78716	Adg78716 Human sec
421	23	100.0	128	6	ABM38028	Abm38028 Propionib	494	23	100.0	142	5	ABP00170	Abp00170 Human ORF
422	23	100.0	128	7	ADA07369	Ada07369 Human sec	495	23	100.0	142	5	ABP00170	Abp00170 Human ORF
423	23	100.0	129	2	AAW78421	Aaw78421 Antibody	496	23	100.0	142	6	ABM43790	Abm43790 Propionib
424	23	100.0	129	4	AAO10803	Aao10803 Human pol	497	23	100.0	142	6	ABM43790	Abm43790 Propionib
425	23	100.0	129	5	ABU05841	Abu05841 M. tuberc	498	23	100.0	143	5	ABP42507	Abp42507 Human ext
426	23	100.0	129	5	ABR57965	Abbr57965 CH3 domai	499	23	100.0	143	7	ABO38358	Abob38358 Pseudomon
427	23	100.0	129	6	ABR55202	Abrr55202 Amino aci	500	23	100.0	143	7	ABO38358	Abob38358 Pseudomon
428	23	100.0	130	2	AAW78422	Aaw78422 Antibody	501	23	100.0	144	5	ABP00772	Abp00772 Human ORF
429	23	100.0	130	2	ABR10669	Abbr10669 Human pan	502	23	100.0	144	5	ABP00772	Abp00772 Human ORF
430	23	100.0	130	4	AAW92711	Aaw92711 Human dig	503	23	100.0	144	7	ADP60370	Adp60370 Human con
431	23	100.0	130	4	ABR11212	Abbr11212 Human gro	504	23	100.0	145	6	ABU08646	Abu08646 Cuphea ac
432	23	100.0	130	4	AAU66197	Aau66197 Propionib	505	23	100.0	146	2	AAU59740	Aau59740 Human nor
433	23	100.0	130	5	ABP04239	Abp04239 Human ORF	506	23	100.0	146	5	ABR97604	Abbr97604 Novel hum
434	23	100.0	130	5	ABR97978	Abbr97978 CH3 domai	507	23	100.0	146	5	ABR97978	Abbr97978 Human pol
435	23	100.0	130	6	ABM62716	Abm62716 Propionib	508	23	100.0	147	5	ABR97978	Abbr97978 Human pol
436	23	100.0	131	3	AAW61110	Aaw61110 Arabidops	509	23	100.0	147	5	ABP63035	Abp63035 Human pol
437	23	100.0	131	4	AAO03385	Aao03385 Human pol	510	23	100.0	148	4	AAU44948	Aau44948 Propionib
438	23	100.0	131	8	ADP89745	Adp89745 Human Clo	511	23	100.0	148	4	AAU41354	Aau41354 Propionib
439	23	100.0	132	4	AAU64768	Aau64768 Propionib	512	23	100.0	148	4	AAU58749	Aau58749 Propionib
440	23	100.0	132	4	ABR15735	Abbr15735 Human ner	513	23	100.0	148	4	ABG25700	Abg25700 Novel hum
441	23	100.0	132	4	AAU20868	Aau20868 Human nov	514	23	100.0	148	5	ABR54249	Abbr54249 Lactococc
442	23	100.0	132	6	ABM61287	Abm61287 Propionib	515	23	100.0	148	5	ADK36954	Adk36954 Novel hum
443	23	100.0	132	6	ABO00696	Abol00696 Novel hum	516	23	100.0	148	6	ABM41467	Abm41467 Propionib
444	23	100.0	132	6	AAO16348	Aao16348 Zinc fing	517	23	100.0	148	6	ABM37873	Abm37873 Propionib
445	23	100.0	133	4	ABG19982	Abg19982 Novel hum	518	23	100.0	148	6	ABM52268	Abm52268 Propionib
446	23	100.0	133	7	ABO66675	Abol66675 Klebsiell	519	23	100.0	148	6	ADH62347	Adh62347 Rhizomuco
447	23	100.0	133	8	ADN21278	Adn21278 Bacterial	520	23	100.0	148	7	ABO72502	Abol72502 Pseudomon
448	23	100.0	134	3	ABR42969	Abrr42969 Human ORF	521	23	100.0	149	3	AAU10091	Aau10091 Arabidops
449	23	100.0	134	3	ABR09067	Abbr09067 Hepatitis	522	23	100.0	149	3	AAU10091	Aau10091 Arabidops
450	23	100.0	134	4	AAW88513	Aaw88513 Human imm	523	23	100.0	149	4	AAU60258	Aau60258 Novel hum
451	23	100.0	134	4	ABG03311	Abg03311 Novel hum	524	23	100.0	149	4	ABG14138	Abg14138 Novel hum
452	23	100.0	134	5	AAE21243	Aae21243 Human gen	525	23	100.0	149	4	ABG19445	Abg19445 Novel hum
453	23	100.0	134	5	ABR40510	Abrr40510 Human gen	526	23	100.0	149	4	ABG19445	Abg19445 Novel hum
454	23	100.0	134	5	ABR40432	Abrr40432 Human sec	527	23	100.0	149	6	ABM56777	Abm56777 Propionib
455	23	100.0	134	6	ABM65627	Abm65627 Propionib	528	23	100.0	149	7	ABR59786	Abrr59786 Connectiv
456	23	100.0	134	7	ADG77021	Adg77021 Human nuc	529	23	100.0	149	7	ABO83324	Abol83324 Pseudomon
457	23	100.0	134	7	ABO78213	Abol78213 Pseudomon	530	23	100.0	150	4	ABG26030	Abg26030 Novel hum
458	23	100.0	134	7	ABO82543	Abol82543 Pseudomon	531	23	100.0	150	4	ABG26030	Abg26030 Novel hum
459	23	100.0	134	7	ABO75224	Abol75224 Pseudomon	532	23	100.0	152	2	AAV74030	Aav74030 Human pro
460	23	100.0	135	3	AAW6109	Aaw6109 Arabidops	533	23	100.0	152	4	AAW18098	Aaw18098 Peptide #
461	23	100.0	135	4	AAO10990	Aao10990 Human pol	534	23	100.0	152	4	ABM37133	Abm37133 Peptide #
462	23	100.0	135	7	ADB64066	Adb64066 Human pro	535	23	100.0	152	4	AAW30608	Aaw30608 Peptide #
463	23	100.0	136	3	AAG22649	Aag22649 Zea may	536	23	100.0	152	4	ABR22444	Abrr22444 Protein #

537	23	100.0	152	4	AAM70271	Aam70271 Human bon	610	23	100.0	166	3	AAV32311	Aay32311 Corn neut
538	23	100.0	152	4	AAM57851	Aam57851 Human bra	611	23	100.0	166	4	AAM18264	Aam18264 Peptide #
539	23	100.0	152	4	AAM05733	Aam05733 Peptide #	612	23	100.0	166	4	AAM15177	Aam15177 Peptide #
540	23	100.0	152	8	ABO58881	Abos8881 Human gen	613	23	100.0	166	4	ABG68346	Abg68346 Drosophil
541	23	100.0	153	3	AB12146	Ab12146 Hydrophob	614	23	100.0	166	4	ABB34170	Abb34170 Peptide #
542	23	100.0	153	4	AAM25859	Aam25859 Human pro	615	23	100.0	166	4	ABB37296	Abb37296 Peptide #
543	23	100.0	153	6	ABU38866	Abu38866 Protein e	616	23	100.0	166	4	AAM27634	Aam27634 Peptide #
544	23	100.0	153	7	ABO78279	Abu78279 Pseudomon	617	23	100.0	166	4	AAM30756	Aam30756 Peptide #
545	23	100.0	154	4	AB193197	Ab193197 Human pro	618	23	100.0	166	4	AB29001	Abb29001 Peptide #
546	23	100.0	154	7	ABO82559	Abu82559 Pseudomon	619	23	100.0	166	4	AB32047	Abb32047 Peptide #
547	23	100.0	154	7	ABO78086	Abu78086 Pseudomon	620	23	100.0	166	4	AB22585	Abb22585 Protein #
548	23	100.0	155	4	AU49773	Aau49773 Propionib	621	23	100.0	166	4	AAM67343	Aam67343 Human bon
549	23	100.0	155	5	ABB80081	Abb80081 Human X-t	622	23	100.0	166	4	AAM70434	Aam70434 Human bon
550	23	100.0	155	5	AAM49002	Aam49002 Human X-t	623	23	100.0	166	4	AAO09591	Aao09591 Human pol
551	23	100.0	155	6	ABR44238	Ab44238 Human sec	624	23	100.0	166	4	AU42240	Aau42240 Propionib
552	23	100.0	155	6	ABM46292	Abm46292 Propionib	625	23	100.0	166	4	AAM57998	Aam57998 Human bra
553	23	100.0	155	6	ABU63127	Abu63127 Human gro	626	23	100.0	166	4	ABG49006	Abg49006 Human liv
554	23	100.0	155	8	ADP81239	Adp81239 Protein o	627	23	100.0	166	4	ABG52114	Abg52114 Human liv
555	23	100.0	155	8	ADP81237	Adp81237 Protein o	628	23	100.0	166	4	AAM05878	Aam05878 Peptide #
556	23	100.0	156	3	AG32713	Aag32713 Zea mays	629	23	100.0	166	4	AAM02915	Aam02915 Peptide #
557	23	100.0	156	4	AU65539	Aau65539 Propionib	630	23	100.0	166	5	ABG40068	Abg40068 Human pep
558	23	100.0	156	6	ABM62058	Abm62058 Propionib	631	23	100.0	166	5	ABG36981	Abg36981 Human pep
559	23	100.0	156	7	ABO82638	Abu82638 Pseudomon	632	23	100.0	166	6	ABM38759	Abm38759 Propionib
560	23	100.0	157	4	AU600019	Aau60019 Propionib	633	23	100.0	166	7	ABO71493	Abu71493 Pseudomon
561	23	100.0	157	5	ABP73657	Abp73657 Candida a	634	23	100.0	167	3	ABBS3263	Aab3263 Human col
562	23	100.0	157	6	ABM65687	Abm65687 Propionib	635	23	100.0	167	8	ABO54950	Abu54950 Human gen
563	23	100.0	157	6	ABM56538	Abm56538 Propionib	636	23	100.0	168	4	AU30792	Aau30792 Novel hum
564	23	100.0	158	4	AAM15625	Aam15625 Peptide #	637	23	100.0	168	6	ADA54175	Ada54175 Human pro
565	23	100.0	158	4	ABM34630	Abm34630 Peptide #	638	23	100.0	168	6	ABRS6758	Abr56758 Human sec
566	23	100.0	158	4	AAM28123	Aam28123 Peptide #	639	23	100.0	169	7	ADE31068	Ade31068 Human dia
567	23	100.0	158	4	AB29453	Ab29453 Peptide #	640	23	100.0	169	7	ABO83162	Abu83162 Pseudomon
568	23	100.0	158	4	ABB20040	Abb20040 Protein #	641	23	100.0	169	7	ABO72246	Abu72246 Pseudomon
569	23	100.0	158	4	ABM67816	Abm67816 Human bon	642	23	100.0	169	7	ABO76458	Abu76458 Pseudomon
570	23	100.0	158	4	AAM55420	Aam55420 Human bra	643	23	100.0	169	7	ABO77823	Abu77823 Pseudomon
571	23	100.0	158	4	ABG49453	Abg49453 Human liv	644	23	100.0	169	7	ABO74253	Abu74253 Pseudomon
572	23	100.0	158	4	AAM03368	Aam03368 Peptide #	645	23	100.0	169	7	ABO76000	Abu76000 Pseudomon
573	23	100.0	158	5	ABG37358	Abg37358 Human pep	646	23	100.0	170	2	AAR10685	Aar10685 TNF and 1
574	23	100.0	159	3	AG35191	Aag35191 Zea mays	647	23	100.0	170	7	ABO75068	Abu75068 Pseudomon
575	23	100.0	159	4	ABG20866	Abg20866 Novel hum	648	23	100.0	170	7	ABO72923	Abu72923 Pseudomon
576	23	100.0	159	6	ABU40159	Abu40159 Protein e	649	23	100.0	170	7	ABO60818	Abu60818 Klebsiell
577	23	100.0	159	7	ABO71251	Abu71251 Pseudomon	650	23	100.0	171	4	AU63745	Aau63745 Propionib
578	23	100.0	160	3	AAY53941	Aay53941 A partial	651	23	100.0	171	4	ABG22251	Abg22251 Novel hum
579	23	100.0	160	3	ABU40913	Abu40913 Human ORF	652	23	100.0	171	6	ABM60264	Abm60264 Propionib
580	23	100.0	160	4	AU49924	Aau49924 Propionib	653	23	100.0	171	7	ABO75885	Abu75885 Pseudomon
581	23	100.0	160	5	ABP05876	Abp05876 Human ORF	654	23	100.0	171	8	ADG32615	Adg32615 Cyanophag
582	23	100.0	160	6	ABM46443	Abm46443 Propionib	655	23	100.0	172	4	AU23729	Aau23729 Novel hum
583	23	100.0	160	8	ADS23556	Ads23556 Bacterial	656	23	100.0	172	4	AU18469	Aau18469 Human end
584	23	100.0	161	8	ABO55412	Abu55412 Human gen	657	23	100.0	173	4	AU60428	Aau60428 Propionib
585	23	100.0	162	3	AB33035	Ab33035 Pinus rad	658	23	100.0	173	6	ABM56947	Abm56947 Propionib
586	23	100.0	162	4	AAM39085	Aam39085 Human pol	659	23	100.0	173	8	ADN99372	Adn99372 Novel hum
587	23	100.0	162	4	AU55590	Aau55590 Propionib	660	23	100.0	174	2	AU20786	Aay20786 Human neu
588	23	100.0	162	4	AU51210	Aau51210 Propionib	661	23	100.0	175	3	AAY44484	Aay44484 Human int
589	23	100.0	162	5	ABB89385	Abb89385 Human pol	662	23	100.0	177	4	AU25588	Aau25588 Human G P
590	23	100.0	162	6	ABM47729	Abm47729 Propionib	663	23	100.0	177	8	ADG22280	Adg22280 Cyanophag
591	23	100.0	162	6	ABM65659	Abm65659 Propionib	664	23	100.0	178	4	AU47551	Aau47551 Propionib
592	23	100.0	162	6	ABM62109	Abm62109 Propionib	665	23	100.0	178	6	ABM44070	Abm44070 Propionib
593	23	100.0	162	7	ADB63996	Abd63996 Human pro	666	23	100.0	178	7	ABO80234	Abu80234 Pseudomon
594	23	100.0	162	8	ADRO8530	Adro8530 Human pro	667	23	100.0	179	4	ABG00072	Abg00072 Novel hum
595	23	100.0	163	2	AAY29213	Aay29213 Amino aci	668	23	100.0	179	7	ABO80126	Abu80126 Pseudomon
596	23	100.0	163	6	ABU41993	Abu41993 Protein e	669	23	100.0	180	2	AAY28235	Aay28235 Human int
597	23	100.0	164	4	AU67280	Aau67280 Propionib	670	23	100.0	180	2	AAM85615	Aam85615 Human zcy
598	23	100.0	164	4	AU57621	Aau57621 Propionib	671	23	100.0	180	2	AAY22197	Aay22197 Human EDI
599	23	100.0	164	6	ABM63799	Abm63799 Propionib	672	23	100.0	180	2	AAV41762	Aay41762 Human PRO
600	23	100.0	164	6	ABM54140	Abm54140 Propionib	673	23	100.0	180	2	AAM97350	Aam97350 Interleuk
601	23	100.0	165	2	AAY07481	Aay07481 Human pho	674	23	100.0	180	3	AB33443	Aab33443 Human PRO
602	23	100.0	165	3	AGI18779	Agi18779 Zea mays	675	23	100.0	180	3	AAY44459	Aay44459 Human int
603	23	100.0	165	3	AGG07098	Aag07098 Arabidops	676	23	100.0	180	3	AB44318	Aab44318 Human PRO
604	23	100.0	165	3	AGG33351	Aag33351 Zea mays	677	23	100.0	180	3	AB18671	Abi18671 Amino aci
605	23	100.0	165	3	AGG47460	Aag47460 Arabidops	678	23	100.0	180	3	AB18755	Abi18755 A human i
606	23	100.0	165	4	ABG01533	Abg01533 Novel hum	679	23	100.0	180	3	AB15541	Abi15541 Human imm
607	23	100.0	165	5	ABB80080	Abb80080 Human sec	680	23	100.0	180	3	AAY93973	Aay93973 Amino aci
608	23	100.0	165	5	AAM49001	Aam49001 Human X-t	681	23	100.0	180	3	ABO7686	Abu7686 A human i
609	23	100.0	165	8	ADP47087	Adp47087 Human pho	682	23	100.0	180	3	AAB07592	Aab07592 A human i

683	23	100.0	180	4	AAE10950	Rael0950 Human	Zcy	756	23	100.0	180	7	ADA87026	Novel	hum
684	23	100.0	180	4	AAU12394	Raul12394 Human	PRO	757	23	100.0	180	7	ADA88129	Novel	hum
685	23	100.0	180	4	AAU04950	Aau04950 Human	INT	758	23	100.0	180	7	ADA46517	Novel	hum
686	23	100.0	180	4	AAB49894	Aab49894 Human	PRO	759	23	100.0	180	7	ADA49766	Human	int
687	23	100.0	180	4	AAG50920	Agb50920 Human	PRO	760	23	100.0	180	7	ADB28547	Human	PRO
688	23	100.0	180	4	AAG65242	Agb65242 Human	cel	761	23	100.0	180	7	ADB29099	Human	PRO
689	23	100.0	180	5	AAU99159	Aau99159 Human	cho	762	23	100.0	180	7	ADA77051	Human	PRO
690	23	100.0	180	6	ABB93361	Abb93361 Amino aci		763	23	100.0	180	7	ADA26959	Human	PRO
691	23	100.0	180	6	ABO17838	Abol17838 Novel	hum	764	23	100.0	180	7	ADA88681	Novel	hum
692	23	100.0	180	6	ABO25264	Abol25264 Novel	hum	765	23	100.0	180	7	ADA97686	Human	PRO
693	23	100.0	180	6	ABU81092	Abu81092 Human	PRO	766	23	100.0	180	7	ADB27443	Human	PRO
694	23	100.0	180	6	ABU72270	Abu72270 Novel	hum	767	23	100.0	180	7	ADB23376	Novel	hum
695	23	100.0	180	6	ABU66792	Abu66792 Human	PRO	768	23	100.0	180	7	ADA67067	Human	PRO
696	23	100.0	180	6	ABU84950	Abu84950 Human	sec	769	23	100.0	180	7	ADB22928	Human	PRO
697	23	100.0	180	6	ABU59873	Abu59873 Novel	sec	770	23	100.0	180	7	ADB23701	Human	PRO
698	23	100.0	180	6	ABU61148	Abu61148 Human	PRO	771	23	100.0	180	7	ADA92423	Novel	hum
699	23	100.0	180	6	ABO25063	Abol25063 Human	sec	772	23	100.0	180	7	ADB15486	Human	PRO
700	23	100.0	180	6	ABU89697	Abu89697 Human	int	773	23	100.0	180	7	ADB38738	Novel	hum
701	23	100.0	180	6	ABU80417	Abu80417 Human	sec	774	23	100.0	180	7	ADB38186	Novel	hum
702	23	100.0	180	6	ABU67068	Abu67068 Human	sec	775	23	100.0	180	7	ADB66658	Novel	hum
703	23	100.0	180	6	ABG17974	Abg17974 Human	ful	776	23	100.0	180	7	ADB31990	Human	int
704	23	100.0	180	6	ABU72592	Abu72592 Human	IL-	777	23	100.0	180	7	ADB89738	Human	PRO
705	23	100.0	180	6	ADA45965	Ada45965 Novel	hum	778	23	100.0	180	7	ADB90470	Human	PRO
706	23	100.0	180	6	ADA76396	Ada76396 Human	PRO	779	23	100.0	180	7	ADB39571	Novel	hum
707	23	100.0	180	6	ADA19046	Ada19046 Human	PRO	780	23	100.0	180	7	ADB73976	Human	PRO
708	23	100.0	180	6	ADA43225	Ada43225 Human	int	781	23	100.0	180	7	ADB47194	Novel	hum
709	23	100.0	180	6	ADA61669	Ada61669 Homo sapi		782	23	100.0	180	7	ADB86801	Human	PRO
710	23	100.0	180	6	ADB19454	Adbl19454 Novel	hum	783	23	100.0	180	7	ADB76692	Human	PRO
711	23	100.0	180	6	ADB27995	Adbl27995 Human	PRO	784	23	100.0	180	7	ADB77406	Novel	hum
712	23	100.0	180	6	ADA86474	Ada86474 Novel	hum	785	23	100.0	180	7	ADB34563	Human	PRO
713	23	100.0	180	6	ADB16038	Adbl16038 Human	PRO	786	23	100.0	180	7	ADB35667	Human	PRO
714	23	100.0	180	6	ADA47824	Ada47824 Human	PRO	787	23	100.0	180	7	ADB66893	Human	PRO
715	23	100.0	180	6	ADA67619	Ada67619 Human	PRO	788	23	100.0	180	7	ADB34011	Human	PRO
716	23	100.0	180	6	ADB30626	Adbl30626 Human	PRO	789	23	100.0	180	7	ADB35115	Human	PRO
717	23	100.0	180	6	ADA85922	Ada85922 Novel	hum	790	23	100.0	180	7	ADB36219	Human	PRO
718	23	100.0	180	6	ADA97134	Ada97134 Human	PRO	791	23	100.0	180	7	ADB46614	Novel	hum
719	23	100.0	180	6	ADA79438	Ada79438 Human	PRO	792	23	100.0	180	7	ADC44118	Human	sec
720	23	100.0	180	6	ADA87577	Ada87577 Novel	hum	793	23	100.0	180	7	ADC61878	Human	sec
721	23	100.0	180	6	ADB16779	Adbl6779 Human	PRO	794	23	100.0	180	7	ADC63842	Human	sec
722	23	100.0	180	6	ADA91871	Ada91871 Novel	hum	795	23	100.0	180	7	ADC66942	Human	sec
723	23	100.0	180	6	ADB14934	Adbl14934 Human	PRO	796	23	100.0	180	7	ADC69066	Human	sec
724	23	100.0	180	6	ADA25009	Ada25009 Novel	hum	797	23	100.0	180	7	ADC63126	Human	sec
725	23	100.0	180	6	ADB18895	Adbl18895 Novel	hum	798	23	100.0	180	7	ADC68191	Human	sec
726	23	100.0	180	6	ADA94110	Ada94110 Human	PRO	799	23	100.0	180	7	ADC41511	Human	sec
727	23	100.0	180	6	ADB20006	Adbl20006 Novel	hum	800	23	100.0	180	7	ADC67566	Human	sec
728	23	100.0	180	6	ADB13318	Adbl13318 Human	PRO	801	23	100.0	180	7	ADC62502	Human	sec
729	23	100.0	180	6	ABO43371	Abol43371 Novel	hum	802	23	100.0	180	7	ADC42135	Human	sec
730	23	100.0	180	6	ABO19719	Abol19719 Novel	hum	803	23	100.0	180	7	ADC50487	Novel	hum
731	23	100.0	180	6	ADA12670	Ada12670 Human	sec	804	23	100.0	180	7	ADC72034	Novel	hum
732	23	100.0	180	6	ADA74572	Ada74572 Human	PRO	805	23	100.0	180	7	ADC60013	Novel	hum
733	23	100.0	180	6	ADB24805	Adbl24805 Human	PRO	806	23	100.0	180	7	ADC53020	Novel	hum
734	23	100.0	180	6	ADA82329	Ada82329 Human	PRO	807	23	100.0	180	7	ADC57374	Novel	hum
735	23	100.0	180	6	ADA75292	Ada75292 Human	PRO	808	23	100.0	180	7	ADC60565	Novel	hum
736	23	100.0	180	6	ADA85370	Ada85370 Novel	hum	809	23	100.0	180	7	ADC51040	Novel	hum
737	23	100.0	180	6	ADA84818	Ada84818 Novel	hum	810	23	100.0	180	7	ADC65567	Human	PRO
738	23	100.0	180	6	ADB30074	Adbl30074 Human	PRO	811	23	100.0	180	7	ADC54665	Novel	hum
739	23	100.0	180	6	ADA80602	Ada80602 Human	PRO	812	23	100.0	180	7	ADC53626	Novel	hum
740	23	100.0	180	6	ADA75844	Ada75844 Human	PRO	813	23	100.0	180	7	ADC59149	Novel	hum
741	23	100.0	180	6	ADA47069	Ada47069 Human	PRO	814	23	100.0	180	7	ADC56027	Novel	hum
742	23	100.0	180	6	ADB25365	Adbl25365 Human	PRO	815	23	100.0	180	7	ADC58597	Novel	hum
743	23	100.0	180	6	ADA93541	Ada93541 Human	PRO	816	23	100.0	180	7	ADD03271	Novel	hum
744	23	100.0	180	6	ADB26891	Adbl26891 Human	PRO	817	23	100.0	180	7	ADC90263	Novel	hum
745	23	100.0	180	6	ADB31178	Adbl31178 Human	PRO	818	23	100.0	180	7	ADC69682	Human	PRO
746	23	100.0	180	6	ADA61106	Ada61106 Homo sapi		819	23	100.0	180	7	ADC48571	Human	PRO
747	23	100.0	180	6	ADB24253	Adbl24253 Human	PRO	820	23	100.0	180	7	ADD10100	Human	PRO
748	23	100.0	180	6	ADA96582	Ada96582 Human	PRO	821	23	100.0	180	7	ADD04675	Novel	hum
749	23	100.0	180	6	ADA81154	Ada81154 Human	PRO	822	23	100.0	180	7	ADC80631	Novel	hum
750	23	100.0	180	6	ADA96030	Ada96030 Human	PRO	823	23	100.0	180	7	ADD11138	Human	PRO
751	23	100.0	180	6	ADB26339	Adbl26339 Human	PRO	824	23	100.0	180	7	ADC48019	Human	PRO
752	23	100.0	180	6	ADB21824	Adbl21824 Novel	hum	825	23	100.0	180	7	ADC80079	Novel	hum
753	23	100.0	180	6	ABO19610	Abol19610 Novel	hum	826	23	100.0	180	7	ADD09548	Human	PRO
754	23	100.0	180	7	ADA77603	Ada77603 Human	PRO	827	23	100.0	180	7	ADB41261	Novel	hum
755	23	100.0	180	7	ADB18343	Adbl18343 Human	PRO	828	23	100.0	180	7	ADD52400	Human	PRO

829	23	100.0	180	7	ADD531140	Ad531140 Human PRO	902	23	100.0	180	8	ADE89309	Human PRO
830	23	100.0	180	7	ADD53692	Ad53692 Novel hum	903	23	100.0	180	8	ADE18448	Human PRO
831	23	100.0	180	7	ADD51848	Ad51848 Human PRO	904	23	100.0	180	8	ADE88757	Human PRO
832	23	100.0	180	7	ADD02647	Ad02647 Human PRO	905	23	100.0	180	8	ADE89905	Human sec
833	23	100.0	180	7	ADD02081	Ad02081 Human PRO	906	23	100.0	180	8	ADF61545	Human sec
834	23	100.0	180	7	ADD54263	Ad54263 Novel hum	907	23	100.0	180	8	ADF40237	Human sec
835	23	100.0	180	7	ADD49504	Ad49504 Human sec	908	23	100.0	180	8	ADF46033	Human sec
836	23	100.0	180	7	ADD92580	Ad92580 Human PRO	909	23	100.0	180	8	ADF46033	Human PRO
837	23	100.0	180	7	ADD91476	Ad91476 Human PRO	910	23	100.0	180	8	ADF46033	Human PRO
838	23	100.0	180	7	ADD04090	Ad04090 Human PRO	911	23	100.0	180	8	ADF46033	Human PRO
839	23	100.0	180	7	ADD32387	Ad32387 Novel hum	912	23	100.0	180	8	ADF46033	Human PRO
840	23	100.0	180	7	ADD22319	Ad22319 Human PRO	913	23	100.0	180	8	ADF46033	Human PRO
841	23	100.0	180	7	ADD79543	Ad79543 Human PRO	914	23	100.0	180	8	ADF46033	Human sec
842	23	100.0	180	7	ADD35558	Ad35558 Human sec	915	23	100.0	180	8	ADF46033	Human sec
843	23	100.0	180	7	ADD16672	Ad16672 Human sec	916	23	100.0	180	8	ADF46033	Human sec
844	23	100.0	180	7	ADD73287	Ad73287 Human sec	917	23	100.0	180	8	ADF46033	Human PRO
845	23	100.0	180	7	ADD42079	Ad42079 Human PRO	918	23	100.0	180	8	ADF46033	Human sec
846	23	100.0	180	7	ADD17896	Ad17896 Human PRO	919	23	100.0	180	8	ADF46033	Human sec
847	23	100.0	180	7	ADD92028	Ad92028 Human PRO	920	23	100.0	180	8	ADF46033	Human sec
848	23	100.0	180	7	ADD33491	Ad33491 Novel hum	921	23	100.0	180	8	ADF46033	Human sec
849	23	100.0	180	7	ADD34043	Ad34043 Novel hum	922	23	100.0	180	8	ADF46033	Human sec
850	23	100.0	180	7	ADD80095	Ad80095 Human PRO	923	23	100.0	180	8	ADF46033	Human sec
851	23	100.0	180	7	ADD93132	Ad93132 Human PRO	924	23	100.0	180	8	ADF46033	Human sec
852	23	100.0	180	7	ADD72645	Ad72645 Human sec	925	23	100.0	180	8	ADF46033	Human sec
853	23	100.0	180	7	ADD19552	Ad19552 Human PRO	926	23	100.0	180	8	ADF46033	Human sec
854	23	100.0	180	7	ADD19000	Ad19000 Human PRO	927	23	100.0	180	8	ADF46033	Human sec
855	23	100.0	180	7	ADD43196	Ad43196 Human PRO	928	23	100.0	180	8	ADF46033	Human sec
856	23	100.0	180	7	ADD95985	Ad95985 Human PRO	929	23	100.0	180	8	ADF46033	Human PRO
857	23	100.0	180	7	ADD22871	Ad22871 Human PRO	930	23	100.0	180	8	ADF46033	Human PRO
858	23	100.0	180	7	ADD78989	Ad78989 Human PRO	931	23	100.0	180	8	ADF46033	Human PRO
859	23	100.0	180	7	ADD32939	Ad32939 Novel hum	932	23	100.0	180	8	ADF46033	Human PRO
860	23	100.0	180	7	ADD42631	Ad42631 Human PRO	933	23	100.0	180	8	ADF46033	Human PRO
861	23	100.0	180	7	ADD17296	Ad17296 Human sec	934	23	100.0	180	8	ADF46033	Human PRO
862	23	100.0	180	7	ADD80647	Ad80647 Human PRO	935	23	100.0	180	8	ADF46033	Human PRO
863	23	100.0	180	7	ADD89675	Ad89675 Human PRO	936	23	100.0	180	8	ADF46033	Human PRO
864	23	100.0	180	7	ADD40959	Ad40959 Human PRO	937	23	100.0	180	8	ADF46033	Human PRO
865	23	100.0	180	7	ADD04758	Ad04758 Human PRO	938	23	100.0	180	8	ADF46033	Human PRO
866	23	100.0	180	7	ABW02053	Abw02053 Human IL-	939	23	100.0	180	8	ADG13395	Human PRO
867	23	100.0	180	7	ADD92887	Ad92887 Human PRO	940	23	100.0	180	8	ADG13395	Human PRO
868	23	100.0	180	7	ADP47310	Adp47310 Human sec	941	23	100.0	180	8	ADG13395	Human PRO
869	23	100.0	180	7	ADG21596	Adg21596 Novel hum	942	23	100.0	180	8	ADG13395	Human PRO
870	23	100.0	180	7	ADG23237	Adg23237 Novel hum	943	23	100.0	180	8	ADG13395	Human PRO
871	23	100.0	180	7	ADG97572	Adg97572 Human PRO	944	23	100.0	180	8	ADG13395	Human PRO
872	23	100.0	180	7	ADG87377	Adg87377 Human PRO	945	23	100.0	180	8	ADG13395	Human PRO
873	23	100.0	180	7	ADG80636	Adg80636 Human PRO	946	23	100.0	180	8	ADG13395	Human PRO
874	23	100.0	180	7	ADG53067	Adg53067 Human sec	947	23	100.0	180	8	ADG13395	Human PRO
875	23	100.0	180	7	ADG60387	Adg60387 Human sec	948	23	100.0	180	8	ADG13395	Human PRO
876	23	100.0	180	7	ADG80084	Adg80084 Human PRO	949	23	100.0	180	8	ADG13395	Human PRO
877	23	100.0	180	7	ADH55376	Adh55376 Novel hum	950	23	100.0	180	8	ADG13395	Human PRO
878	23	100.0	180	7	ADH55928	Adh55928 Novel hum	951	23	100.0	180	8	ADG13395	Human PRO
879	23	100.0	180	7	ADI61147	Adi61147 Human sec	952	23	100.0	180	8	ADG13395	Human PRO
880	23	100.0	180	7	ADI64147	Adi64147 Novel hum	953	23	100.0	180	8	ADG13395	Human PRO
881	23	100.0	180	7	ADI65096	Adi65096 Novel hum	954	23	100.0	180	8	ADG13395	Human PRO
882	23	100.0	180	7	ADH82009	Adh82009 Novel hum	955	23	100.0	180	8	ADG13395	Human PRO
883	23	100.0	180	7	ADH81457	Adh81457 Novel hum	956	23	100.0	180	8	ADG13395	Human PRO
884	23	100.0	180	7	ADL16673	Adl16673 Human PRO	957	23	100.0	180	8	ADG13395	Human PRO
885	23	100.0	180	7	ADM82626	Adm82626 Novel hum	958	23	100.0	180	8	ADG13395	Human PRO
886	23	100.0	180	7	ADN16025	Adn16025 Novel hum	959	23	100.0	180	8	ADG13395	Human PRO
887	23	100.0	180	7	ADN16654	Adn16654 Novel hum	960	23	100.0	180	8	ADG13395	Human PRO
888	23	100.0	180	7	ADN15473	Adn15473 Novel hum	961	23	100.0	180	8	ADG13395	Human PRO
889	23	100.0	180	7	ADN14921	Adn14921 Novel hum	962	23	100.0	180	8	ADG13395	Human PRO
890	23	100.0	180	7	ABO74034	Ab074034 Pseudomon	963	23	100.0	180	8	ADG13395	Human PRO
891	23	100.0	180	7	ADI63595	Adi63595 Novel hum	964	23	100.0	180	8	ADG13395	Human PRO
892	23	100.0	180	8	ADC81183	Adc81183 Novel hum	965	23	100.0	180	8	ADG13395	Human PRO
893	23	100.0	180	8	ADD76631	Ad76631 Human PRO	966	23	100.0	180	8	ADG13395	Human PRO
894	23	100.0	180	8	ADD87995	Ad87995 Human PRO	967	23	100.0	180	8	ADG13395	Human PRO
895	23	100.0	180	8	ADD86399	Ad86399 Human PRO	968	23	100.0	180	8	ADG13395	Human PRO
896	23	100.0	180	8	ADP75847	Adp75847 Human PRO	969	23	100.0	180	8	ADG13395	Human PRO
897	23	100.0	180	8	ADE48804	Ad48804 Human sec	970	23	100.0	180	8	ADG13395	Human PRO
898	23	100.0	180	8	ADE23423	Ad23423 Human PRO	971	23	100.0	180	8	ADG13395	Human PRO
899	23	100.0	180	8	ADE23975	Ad23975 Human PRO	972	23	100.0	180	8	ADG13395	Human PRO
900	23	100.0	180	8	ADE24618	Ad24618 Human PRO	973	23	100.0	180	8	ADG13395	Human PRO
901	23	100.0	180	8	ADD87443	Ad87443 Human PRO	974	23	100.0	180	8	ADG13395	Human PRO

975 23 100.0 180 8 ADG61539 Novel hum
 976 23 100.0 180 8 ADH28626 Human PRO
 977 23 100.0 180 8 ADG54771 Novel hum
 978 23 100.0 180 8 ADG59811 Novel hum
 979 23 100.0 180 8 ADG51267 Novel hum
 980 23 100.0 180 8 ADG59211 Human sec
 981 23 100.0 180 8 ADG62667 Human sec
 982 23 100.0 180 8 ADI81235 Human PRO
 983 23 100.0 180 8 ADH25692 Human neu
 984 23 100.0 180 8 ADG09978 Novel hum
 985 23 100.0 180 8 ADI15449 Novel hum
 986 23 100.0 180 8 ADG09326 Novel hum
 987 23 100.0 180 8 ADI14781 Novel hum
 988 23 100.0 180 8 ADI18376 Novel hum
 989 23 100.0 180 8 ADJ61725 Human int
 990 23 100.0 180 8 ADL16634 Human PRO
 991 23 100.0 180 8 ADL71294 Human IL-
 992 23 100.0 180 8 ADJ63657 Novel hum
 993 23 100.0 180 8 ADJ77552 Human PRO
 994 23 100.0 180 8 ADJ65674 Human PRO
 995 23 100.0 180 8 ADM27810 Human PRO
 996 23 100.0 180 8 ADM17469 Human sec
 997 23 100.0 180 8 ADL07303 Human sec
 998 23 100.0 180 8 ADM42534 Human PRO
 999 23 100.0 180 8 ADM28396 Human PRO
 1000 23 100.0 180 8 ADL13792 Human int

ALIGNMENTS

RESULT 1
 AAB07766
 ID AAB07766 standard; peptide; 4 AA.
 XX
 AC AAB07766;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Peptide which is not present in arginine-proline peptides.
 XX
 KW Pro-inflammatory cytokine; interleukin; IL-6; IL-8; fibroblast;
 KW keratinocyte; cosmetic; dermatological composition;
 KW immunological dysfunction; skin; inflammation; aging; ultra-violet light.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "this residue is H-Thr"
 FT FT
 FT Misc-difference 4 /note= "this residue is Arg-OH"
 FT FT
 XX WO200043417-A1.
 PN
 XX
 XX 27-JUL-2000.
 PD
 XX
 PF 06-JAN-2000; 2000WO-FR000031.
 XX
 XX 22-JAN-1999; 99FR-00000743.
 PR
 XX (SEDE-) SEDERMA.
 PA
 XX Lintrner K;
 PI
 XX WPI; 2000-505831/45.
 DR
 XX New arginine-proline peptides, useful in cosmetics and dermatology for
 PT treating e.g. inflammation, inhibit overproduction of proinflammatory
 PT interleukins.
 XX
 XX Claim 5; Page 10; 20pp; French.
 PS
 XX

CC The specification describes peptides which contain a proline and a
 CC terminal arginine residue. The proviso is that the peptides are not
 CC AAB07765-68 and AAB07801. The proviso is that the invention restore (and
 CC reduce) the levels of the pro-inflammatory cytokines interleukin (IL)-6
 CC and IL-8 to levels found in young tissue (fibroblasts and keratinocytes).
 CC The peptides are useful in cosmetic and dermatological compositions for
 CC prevention or treatment of immunological dysfunction of the skin, and
 CC inflammation caused by physiological aging and normal exposure to ultra-
 CC violet light
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 23; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 1 GQPR 4
 RESULT 2
 AAB92377
 ID AAB92377 standard; peptide; 4 AA.
 XX
 AC AAB92377;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Miscellaneous peptide SEQ ID NO:1553.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 XX WPI; 2001-112059/12.
 DR
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PT
 XX Disclosure; Page 712; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 23; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 1 GQPR 4

RESULT 3

ADJ81639
 ID ADJ81639 standard; peptide; 4 AA.

XX AC ADJ81639;

XX DT 06-MAY-2004 (first entry)

XX DE Dermatological composition #1.

XX dermatological; angiotensin converting enzyme inhibitor; cosmetic;
 KW topical use; hesperidin; angiotensin converting enzyme; facial skin.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "optionally modified with palmitoyl group"
 FT

XX WO2003068141-A2.

XX PD 21-AUG-2003.

XX PF 10-FEB-2003; 2003WO-FR000441.

XX PR 15-FEB-2002; 2002FR-00001967.

XX (SEDE-) SEDERMA.

XX PI Linthner K;

XX WPI; 2003-778888/73.

XX Cosmetic or dermatological compositions, useful for the treatment of bags
 PT under the eyes, comprise at least two of hesperidin or its derivatives,
 PT angiotensin converting enzyme (ACE)-inhibiting dipeptides and proline-
 PT arginine oligopeptides.

XX Claim 5; Page 23; 26pp; French.

XX The invention relates to novel cosmetic or dermatological compositions
 CC for topical use comprising at least two components selected from
 CC hesperidin or its derivatives, angiotensin converting enzyme (ACE)-
 CC inhibiting dipeptides and oligopeptides with a C-terminal prolyl-arginine
 CC motif. The compositions are useful for the treatment of facial skin,
 CC especially bags under the eyes, preferably by continuous topical delivery
 CC from particles, capsules, fabrics or clothing in direct contact with the
 CC skin or hair. This sequence represents an example of the compositions of
 CC the invention.

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 23; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||

Db 1 GQPR 4

RESULT 4

ADN03394
 ID ADN03394 standard; peptide; 4 AA.

XX AC ADN03394;

XX DT 17-JUN-2004 (first entry)

XX DE Exemplary peptide ligand for proteome analysis #120.

XX Peptide ligand; proteome; capture compound; mass spectrometry;

KW protein separation;

KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.

XX OS Unidentified.

XX US2003119021-A1.

XX PD 26-JUN-2003.

XX PF 16-JUL-2002; 2002US-00197954.

XX PR 16-JUL-2001; 2001US-0306019P.

XX PR 21-AUG-2001; 2001US-0314123P.

XX PR 11-MAR-2002; 2002US-0363433P.

XX (KOST/) KOSTER H.

PA (SIDD/) SIDDIQI S.

PA (LITT/) LITTLE D P.

XX PI Koster H, Siddiqi S, Little DP;

XX WPI; 2004-059185/06.

XX Collection of capture compounds capable of binding to biomolecules to
 PT form complexes that are stable under mass spectrometry conditions, useful
 PT for analysis of biomolecules, especially proteins.

XX Disclosure; SEQ ID NO 120; 165pp; English.

XX The invention relates to a collection of capture compounds capable of
 CC binding to biomolecules to form complexes that are stable under mass
 CC spectrometry conditions. The formulae for the capture compounds comprises
 CC sets of compounds of formula (I)-(III) given in the specification. Also
 CC included are analysis of biomolecules (by contacting a composition
 CC comprising a biomolecule with the above collection and identifying or
 CC detecting bound biomolecules), separating protein conformers (by
 CC contacting a composition comprising a biomolecule with the above
 CC collection, separating the members of the collection and identifying
 CC bound proteins), reducing diversity of a complex mixture of biomolecules
 CC (by contacting the mixture with the above collection and separating each
 CC set of complexes of capture compounds with biomolecules from the other
 CC sets) and identifying phenotype-specific biomolecules (by sorting cells
 CC from a single subject into sets according to a phenotype, contacting
 CC mixtures of biomolecules from each set with the above collection and
 CC comparing the patterns of biomolecule binding from each set). The
 CC collection of capture compounds is useful for the analysis of
 CC biomolecules, especially proteins (e.g. analysis of a proteome), using
 CC mass spectrometry, especially matrix assisted laser desorption ionisation
 CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
 CC exemplary peptide ligand which may be incorporated into a capture
 CC compound of the invention.

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 23; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4


```

Db          |||||
            1 GQPR 4

RESULT 7
ADR42229
ID  ADR42229 standard; peptide; 4 AA.
XX  ADR42229;
AC  ADR42229;
XX  ADR42229;
DT  21-OCT-2004 (first entry)
XX  Rigin related peptide ligand, SEQ ID 120.
XX  Human; ligand; Rigin.
XX  Homo sapiens.
OS  Homo sapiens.
XX  WO2004064972-A2.
PN  WO2004064972-A2.
PD  05-AUG-2004.
XX  05-AUG-2004.
XX  16-JAN-2004; 2004WO-US001037.
XX  16-JAN-2003; 2003US-0441398P.
XX  (HKPH-) HK PHARM INC.
XX  (KOE/) KOESTER H.
XX  Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;
PI  Haseman CF, Yip P;
XX  WPI; 2004-642213/62.
XX  Identifying drug non-target biomolecules in mixture of biomolecules
PT  involves interacting mixture of biomolecules with capture compounds
PT  having high binding affinity and analyzing captured biomolecules to
PT  identify drug non-targets.
XX  Disclosure; SEQ ID NO 120; 368pp; English.
XX  The present invention relates to a method for identifying drug non-target
CC  biomolecules in a mixture of biomolecules. The method comprises
CC  interacting mixture with capture compounds having moiety X which
CC  covalently binds to biomolecules with high affinity, moiety Y that
CC  increases selectivity of binding so that the capture compound binds to
CC  fewer biomolecules, and moiety Z for presenting X and Y, and analysing
CC  captured biomolecules to identify drug non-targets. The capture compound
CC  also optionally comprises a sorting function moiety Q and or a solubility
CC  function moiety W. The selectivity function moiety Y serves to modulate
CC  the reactivity function by reducing the number of groups to which the
CC  reactivity function moiety X bind, such as by steric hindrance and other
CC  interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).
XX  SQ  Sequence 4 AA;
      Query Match 100.0%; Score 23; DB 8; Length 4;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GQPR 4
    |||||
Db  1 GQPR 4

RESULT 8
AAY02344
ID  AAY02344 standard; peptide; 9 AA.
XX  AAY02344;
AC  AAY02344;
XX  AAY02344;
DT  09-JUL-1999 (first entry)
XX  AAY02344;

Peptide used to screen EST databases to identify heparinase DNA sequence.
Heparanase; hp; modulator; heparin-binding growth factor;
cellular response; cytokine; cell interaction; plasma lipoprotein;
cellular susceptibility; infection; disintegration;
neurodegenerative plaque; wound healing; angiogenesis; restenosis;
atherosclerosis; inflammation; neurodegenerative disease; neurallise;
plasma heparin; micrometastasis; autoimmune lesion; renal failure.
XX  Synthetic.
XX  WO9911798-A1.
XX  11-MAR-1999.
XX  31-AUG-1998; 98WO-US017954.
XX  02-SEP-1997; 97US-00922170.
XX  02-JUL-1998; 98US-00109386.
XX  (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX  (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX  (FRIE/) FRIEDMAN M M.
XX  Pecker I, Vlodavsky I, Feinstein E;
XX  WPI; 1999-302255/25.
XX  New human polynucleotide useful for treating angiogenesis, restenosis,
PT  and inflammation.
XX  Example 1; Page 25; 63pp; English.
XX  The specification describes a polypeptide having heparanase (hp)
CC  activity. The recombinant protein is used as a modulator of heparin-
CC  binding growth factors, cellular responses to heparin-binding growth
CC  factors and cytokines, cell interaction with plasma lipoproteins,
CC  cellular susceptibility to viral, protozoal and bacterial infections or
CC  disintegration of neurodegenerative plaques. Heparanase may be useful for
CC  conditions such as wound healing, angiogenesis, restenosis,
CC  atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC  infections. Mammalian heparanase can be used to neutralize plasma
CC  heparin, and anti-heparanase antibodies may be applied for
CC  immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC  renal failure in biopsy specimens, plasma samples, and body fluids. The
CC  present sequence represents a sequence used in the course of the
CC  invention
XX  SQ  Sequence 9 AA;
      Query Match 100.0%; Score 23; DB 2; Length 9;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GQPR 4
    |||||
Db  6 GQPR 9

RESULT 9
AAB08848
ID  AAB08848 standard; peptide; 9 AA.
XX  AAB08848;
AC  AAB08848;
XX  AAB08848;
DT  15-JAN-2001 (first entry)
XX  AAB08848;
DE  Peptide found in protein encoded by ESTs related to heparanase cDNA.
XX  Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
XX  heparin-binding growth factor; cytokine; neurodegenerative plaque;
XX  wound healing; infection; burn; angiogenesis; restenosis;
XX  atherosclerosis; inflammation; neurodegenerative disease;

```


PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
 PT a polypeptide with heparanase activity, useful for treating diseases such
 as cancer and autoimmune disorders.

PS Example 1; SEQ ID NO 8; 108pp; English.

XX The invention relates to an antisense oligonucleotide (ASO) comprising a
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being
 CC hybridizable in vivo, under physiological conditions, with a portion of
 CC a polynucleotide strand encoding a polypeptide having heparanase
 CC catalytic activity. Also included are a method of in vivo downregulating
 CC heparanase activity (comprising administering the ASO in vivo), a method
 CC of treating a subject suffering from a pathological condition
 CC (characterised by heparanase activity, comprising administering ASO to
 CC the subject), a pharmaceutical composition comprising the ASO and a
 CC carrier, an antisense nucleic acid construct (comprising a promoter
 CC sequence and a polynucleotide sequence directing the synthesis of an
 CC antisense RNA sequence of at least 10 bases being hybridizable in vivo,
 CC under physiological conditions, with a polynucleotide strand encoding a
 CC polypeptide having heparanase catalytic activity), a method of in vivo
 CC downregulating heparanase activity (comprising administering in vivo the
 CC antisense nucleic acid construct), a pharmaceutical composition
 CC comprising the antisense nucleic acid construct and a carrier, and an
 CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
 CC analogue of at least 10 bases being hybridizable in vivo, under
 CC physiological conditions, with a portion of a polynucleotide strand being
 CC characterised by forming at least a portion of an untranslated region
 CC (UTR) for a polynucleotide strand encoding a polypeptide having
 CC heparanase catalytic activity. The methods and compositions of the
 CC present invention are useful for the prevention and/or treatment of
 CC diseases or conditions associated with aberrant heparanase activity, such
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and
 CC inflammation. The present sequence is a human heparanase tryptic peptide
 CC used to design primers for cDNA isolation.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GQPR 4
 Db |||||
 6 GQPR 9

RESULT 12
 ADM48714
 ID ADM48714 standard; protein; 9 AA.

XX AC ADM48714;

XX DT 03-JUN-2004 (first entry)

XX DE Human hpa protein tryptic peptide.

XX KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
 KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
 KW human.

XX OS Homo sapiens.

XX PN US2003217375-A1.

XX PD 20-NOV-2003.

XX PF 24-FEB-2003; 2003US-00371218.

XX PR 31-AUG-1998; 98WO-US017954.

XX PR 01-MAR-1999; 99US-00258892.

XX PR 06-FEB-2001; 2001US-00776874.

XX PR 19-NOV-2001; 2001US-00988113.

XX

(ZCHA/) ZCHARIA E.
 (VLOD/) VLODAVSKY I.
 (METZ/) METZGER S.
 (PECK/) PECKER I.
 (ILAN/) ILAN N.
 (CHAJ/) CHAJEK-SHAUL T.
 (GOLD/) GOLDSCHMIDT O.

Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;

Chajek-Shaul T, Goldschmidt O;

WPI; 2004-021918/02.

XX New transgenic non-human animal expressing heparinase, useful as models
 PT for human disease, such as cancers, viral infection, neurodegenerative
 PT diseases, restenosis, atherosclerosis and pulmonary disorders.

PS Example 1; SEQ ID NO 8; 106pp; English.

XX The present invention relates to a transgenic non-human animal whose
 CC genome comprises an exogenous polynucleotide sequence, including a
 CC promoter active in tissues of the non-human, a region encoding a human
 CC heparanase, where the promoter and the region encoding human heparanase
 CC are operably linked in the exogenous polynucleotide such that human
 CC heparanase is expressed in at least a portion of the cells of the non-
 CC human animal. The methods and compositions of the present invention are
 CC useful for the production of transgenic animals expressing heparanase, to
 CC be used as models for human diseases such as cancers, viral infection,
 CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
 CC disorders. The present sequence is human hpa protein tryptic peptide used
 CC in the exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GQPR 4
 Db |||||
 6 GQPR 9

RESULT 13

AAY34181

ID AAY34181 standard; peptide; 10 AA.

XX AC AAY34181;

XX DT 15-NOV-1999 (first entry)

XX DE Human pre-proheparanase protein sequence fragment #8.

XX KW Human; pre-proheparanase; platelet; wound healing; angiogenesis blocker;
 KW inflammation; psoriasis; diabetic retinopathy; solid tumour; arthritis;
 KW heparin degradation; anticoagulant neutralisation; asthma; CNS disease;
 KW inflammatory disease; vascular restenosis; atherosclerosis; diagnosis;
 KW tumour growth; fibroproliferative disorder; neurodegenerative disease;
 KW therapy.

XX OS Homo sapiens.

XX PN WO9943830-A2.

XX PD 02-SEP-1999.

XX PF 18-FEB-1999; 99WO-US001489.

XX PR 24-FEB-1998; 98US-0075706P.

XX PR 26-MAR-1998; 98US-0079401P.

XX (PHAA) PHARMACIA & UPJOHN CO.

Query Match 100.0%; Score 23; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 8 GQPR 11

RESULT 16
ABU03391
ID ABU03391 standard; protein; 11 AA.
XX
AC ABU03391;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #171.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
PS WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Claim 10; SEQ ID NO 171; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 23; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 8 GQPR 11

RESULT 17
ADD23535
ID ADD23535 standard; peptide; 11 AA.
XX
AC ADD23535;
XX
DT 15-JAN-2004 (first entry)
XX
DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:271.
XX
KW breast cancer; screening; diagnosis; breast cancer therapy;
KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003087831-A2.
XX
PD 23-OCT-2003.
XX
PF 10-APR-2003; 2003WO-GB001559.
XX
PR 11-APR-2002; 2002GB-00008331.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Hudson LJ, Stamps AC, Terrett JA;
XX
DR WPI; 2003-845381/78.
XX
PT Screening, diagnosing and/or treating breast cancer by detecting a change
PT in expression or activity of a breast cancer membrane protein (BCMP)
PT polypeptide or encoding nucleic acid molecule.
XX
PS Claim 1; SEQ ID NO 271; 81pp; English.
XX
CC The present invention describes a method of screening for and/or
CC diagnosing breast cancer in a subject, and/or monitoring the
CC effectiveness of breast cancer therapy. The method comprises detecting
CC and/or quantifying in a biological sample obtained from the subject a
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
CC molecule. Also described: (1) an antibody, its functionally-active
CC fragment, derivative or analogue, that specifically binds to one or more
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
CC reagent specific for an BCMP polypeptide, reagents and instructions for
CC use; (3) a method for screening for anti-breast cancer agents that
CC interact with the BCMP polypeptide, comprising contacting the polypeptide
CC with a candidate agent, and determining whether or not the candidate
CC agent interacts with the polypeptide; (4) a method for screening for anti
CC -breast cancer agents that modulate the expression or activity of an BCMP
CC polypeptide or the nucleic acid molecule cited above, comprising
CC comparing the expression or activity of the polypeptide or nucleic acid
CC molecule, in the presence and absence of a candidate agent or in the
CC presence of a control agent, and determining whether the candidate agent
CC causes the expression or activity of the polypeptide or nucleic acid
CC molecule to change; and (5) an agent identified by the method of (3) or
CC (4), which interacts with the polypeptide or causes the expression or
CC activity of the polypeptide, or the expression of the nucleic acid
CC molecule to change. BCMPs have cytostatic activities, and can be used in
CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
CC their derivatives, are useful in the manufacture of a medicament for the
CC treatment of breast cancer, where the composition is a vaccine. The
CC present sequence represents a BCMP peptide which is used in the
CC exemplification of the present invention.

```
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 23; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 8 GQPR 11

RESULT 18
AAU87007
ID AAU87007 standard; peptide; 12 AA.
XX
AC AAU87007;
XX
DT 21-MAY-2002 (first entry)
XX
DE Estradiol mimotope peptide #55.
XX
KW Estradiol; mimotope; estrone-3-glucuronide; steroid detection;
KW immunoassay; phage display; immunogen.
XX
OS Synthetic.
XX
PN WO200212270-A1.
XX
PD 14-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-EP008705.
XX
PR 03-AUG-2000; 2000EP-00306613.
XX
XX (UNIL ) UNILEVER PLC.
PA (UNIL ) UNILEVER NV.
PA (UNIL ) HINDUSTAN LEVER LTD.
XX
PI Badley RA, Berry MJ, Williams SC;
XX
XX WPI; 2002-241729/29.
XX
Peptide mimotope capable of binding specifically to antibody specific to
estradiol, useful for assaying presence and/or amount of estradiol,
especially estrone-3-glucuronide in sample.
XX
Claim 3; Page 27; 57pp; English.
XX
The invention relates to a purified peptide mimotope capable of binding
specifically to an antibody specific to estradiol. Also included are a
solid support having immobilised (releasably or non-releasably) peptide
mimotopes, an immunoassay test device for the detection of estradiol in
the sample, comprising the mimotopes and an antibody capable of binding
specifically to the mimotopes to generate a detectable signal and an
isolated nucleic acid encoding the peptide mimotopes. The mimotope is
useful for assaying the presence and/or amount of estradiol preferably
estrone-3-glucuronide in a sample which is urine or serum sample to be
tested and is also utilised in an immunoassay test device, and further
can be used as immunogens. The mimotope be used to construct new, or
improve the performance of old, immunoassay test formats and devices.
They can, for example, be utilised essentially to tune the signal in
conventional displacement assays for the detection of estradiol. The
mimotope can be bound directly to certain assay surfaces which are
otherwise non-compatible with estradiol on such surfaces needing to be
bound to the surface by complexing with another - often proteinaceous -
molecule. The mimotope is capable of being bound to the antigen-binding
site of an antibody in a selective fashion in the presence of excess
quantities of other undesired materials, and tightly enough (i.e. with
high enough affinity) that when used in an immunoassay, it provides a
useful result). The present sequence is a peptide mimotopes of the
invention
XX
```

```
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 23; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 5 GQPR 8

RESULT 19
AAP51019
ID AAP51019 standard; protein; 13 AA.
XX
AC AAP51019;
XX
DT 25-MAR-2003 (revised)
DT 16-AUG-2002 (revised)
DT 06-SEP-1991 (first entry)
XX
XX Sequence encoded by the area around the linkage between Ch2 and Ch3 of hC
DE gamma 1.
XX
KW Hybrid immunoglobulin; mouse-human hybrid.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Region 1..6 /label= Ch2
FT Region 7..13 /label= Ch3
FT Region 7..13 /label= Ch3
XX
XX EP162319-A.
PN
XX
PD 27-NOV-1985.
XX
PF 24-APR-1984; 84JP-00082432.
XX
PR 24-APR-1984; 84JP-00082432.
XX
XX (HONG/) HONJO T.
PA
PI Honjo T;
XX
XX WPI; 1985-297774/48.
DR N-PSDB; AAN50019.
XX
XX
Intron free linking of genes of different origins - by inserting into
retrovirus then splicing in eucaryotic cell.
XX
Example; Fig 8d(ii); 30pp; English.
XX
The inventors claim a method for the intron free linking of genes of
different origins. The DNA sequence are esp. mouse and human
immunoglobulin genes; one coding for the variable region and the other
for the constant region. (Updated on 16-AUG-2002 to add missing OS
field.) (Updated on 25-MAR-2003 to correct PD field.)
XX
XX Sequence 13 AA;
Query Match 100.0%; Score 23; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 20
```

```

ABU60996
ID ABU60996 standard; protein; 13 AA.
XX
AC ABU60996;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific protein (LSP) #99.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 11; Page 379; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This is the amino
CC acid sequence of a lung specific nucleic acid
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 23; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 3 GQPR 6
RESULT 21
ID AAM98739 standard; peptide; 14 AA.
XX
AC AAM98739;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #2014 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX
interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 4109; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 23; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 7 GQPR 10
RESULT 22
ID AAP82447 standard; peptide; 15 AA.
XX
AC AAP82447;
XX
DT 10-MAR-2003 (revised)
DT 07-NOV-1990 (first entry)
XX
DE Immune-modulating oligopeptide.
XX
KW Immune system; Ig Fc receptors; rheumatoid arthritis; vasculitis;
KW autoimmune diseases; asthma; immunostimulant.
XX
OS Unidentified.
XX
PN US4752601-A.
XX

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PD 21-JUN-1988.
 XX
 XX
 PF 01-APR-1986; 86US-00846930.
 XX
 PR 12-AUG-1983; 83US-00522739.
 XX
 XX (IMMU-) IMMUNETECH PHARM.
 PA
 XX Hahn GS;
 XX
 XX WPI; 1988-190340/27.
 DR
 XX Modulating immune complex-mediated immune response - by admin. of
 XX oligopeptide to block immune complex binding to immunoglobulin Fc
 PT receptors.
 PT
 XX Claim 1; Page 20; 20pp; English.
 PS
 XX This peptide is administered to mammals to modulate an immune-complex
 CC mediated response. It blocks immune-complex binding to Ig Fc receptors. It
 CC is administered in an amt. sufficient to modulate the proliferation or
 CC function of mononuclear cells or to reduce immune-complex mediated
 CC inflammation or tissue destruction. It is thus useful in the treatment of
 CC e.g. rheumatoid arthritis, glomerulonephritis, asthma, autoimmune
 CC diseases and anaemias. It is also an efficient immunostimulant. Residues
 CC 13-15 may be absent (one or a combination or all three). (Updated on 10-
 CC MAR-2003 to add missing OS field.)
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 7 GQPR 10
 RESULT 23
 AAY13277
 ID AAY13277 standard; peptide; 15 AA.
 AC AAY13277;
 XX
 XX 21-JUN-1999 (first entry)
 DT
 XX Naturally occurring variant of the glutenin epitope Y13221.
 DE
 XX Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
 KW gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
 KW tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
 XX
 XX Synthetic.
 OS
 XX EP905518-A1.
 PN
 XX 31-MAR-1999.
 PD
 XX 23-SEP-1997; 97EP-00202909.
 XX
 XX 23-SEP-1997; 97EP-00202909.
 PR
 XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;
 XX WPI; 1999-192792/17.
 XX
 XX New antigenic peptides of gluten and methods for isolating them, useful
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac
 PT disease (CD).

XX Disclosure; Page 28; 58pp; English.
 PS
 XX Peptides AAY13220-13343 represents gluten derived peptides, and their
 CC variants. The specification describes a method to find and characterize
 CC peptides that are recognized by an intestinally derived gluten-sensitive
 CC T-cells. The method comprises establishing and contacting at least one
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,
 CC and fractionating the mixture to select peptides that stimulate the
 CC clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived
 CC peptide) and AAY13221 (glutenin derived peptide) were identified using
 CC these methods, and can be used in pharmaceuticals/medicines (vaccines)
 CC for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e.
 CC celiac disease (CD) or celiac sprue, tropical sprue, childhood food
 CC allergies and dermatitis herpetiformis (DH). The peptides are also useful
 CC for elimination of a group of gluten-sensitive T-cells, and for
 CC generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by
 CC immunization of a mammal with the peptide
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 1 GQPR 4
 RESULT 24
 AAY13300
 ID AAY13300 standard; peptide; 15 AA.
 XX
 XX AAY13300;
 AC
 XX 21-JUN-1999 (first entry)
 DT
 XX Naturally occurring variant of the glutenin epitope Y13221.
 DE
 XX Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
 KW gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
 KW tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
 XX
 XX Synthetic.
 OS
 XX EP905518-A1.
 PN
 XX 31-MAR-1999.
 PD
 XX 23-SEP-1997; 97EP-00202909.
 PF
 XX 23-SEP-1997; 97EP-00202909.
 PR
 XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;
 XX WPI; 1999-192792/17.
 XX
 XX New antigenic peptides of gluten and methods for isolating them, useful
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac
 PT disease (CD).
 XX
 XX Disclosure; Page 35; 58pp; English.
 PS
 XX Peptides AAY13220-13343 represents gluten derived peptides, and their
 CC variants. The specification describes a method to find and characterize
 CC peptides that are recognized by an intestinally derived gluten-sensitive
 CC T-cells. The method comprises establishing and contacting at least one
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,
 CC and fractionating the mixture to select peptides that stimulate the

CC clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived peptide) and AAY13221 (glutenin derived peptide) were identified using these methods, and can be used in pharmaceuticals/medicines (vaccines) for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e. celiac disease (CD) or celiac sprue, tropical sprue, childhood food allergies and dermatitis herpetiformis (DH). The peptides are also useful for elimination of a group of gluten-sensitive T-cells, and for generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by immunization of a mammal with the peptide

XX Sequence 15 AA;

Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 1 GQPR 4

RESULT 25

AAV13251
ID AAY13251 standard; peptide; 15 AA.

XX AC AAY13251;

DT 21-JUN-1999 (first entry)

XX Naturally occurring variant of the glutenin epitope Y13221.

XX Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
XX Gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
XX Tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.

OS Synthetic.

PN EP905518-A1.

XX 31-MAR-1999.

XX 23-SEP-1997; 97EP-00202909.

XX 23-SEP-1997; 97EP-00202909.

XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

PA (UYLE-) RIJKSUNIV LEIDEN.

XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;

XX WPI; 1999-192792/17.

XX New antigenic peptides of gluten and methods for isolating them, useful as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac disease (CD).

XX Disclosure; Page 21; 58pp; English.

XX Peptides AAY13220-13343 represents gluten derived peptides, and their variants. The specification describes a method to find and characterize peptides that are recognized by an intestinally derived gluten-sensitive T-cells. The method comprises establishing and contacting at least one gluten-sensitive T-cell clone with a mixture of gluten-derived peptides, and fractionating the mixture to select peptides that stimulate the clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived peptide) and AAY13221 (glutenin derived peptide) were identified using these methods, and can be used in pharmaceuticals/medicines (vaccines) for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e. celiac disease (CD) or celiac sprue, tropical sprue, childhood food allergies and dermatitis herpetiformis (DH). The peptides are also useful for elimination of a group of gluten-sensitive T-cells, and for generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by immunization of a mammal with the peptide

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 1 GQPR 4

RESULT 26

ADM08091
ID ADM08091 standard; peptide; 15 AA.

XX AC ADM08091;

DT 20-MAY-2004 (first entry)

XX Canine immunoglobulin group 2 lambda VL species framework 4 peptide 20.

XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; Igs; gene therapy; group 2 lambda species;
XX VL framework; FR4.

XX Canis familiaris.

XX WO2003060080-A2.

XX 24-JUL-2003.

XX 20-DEC-2002; 2002WO-US041362.

XX 21-DEC-2001; 2001US-0344874P.

XX (IDEX-) IDEXX LAB INC.

XX Krah ER, Guo H, Aiyappa A, Lawton R;

XX WPI; 2003-598521/56.

XX New canine heavy and light chain variable domain polypeptides, useful for treating canine allergy.

XX Claim 34; Page 102; 130pp; English.

XX The invention relates to a novel canine heavy or light chain variable domain polypeptide. The protein of the invention demonstrates CC antiallergic activity and may be useful for treating canine allergy, CC possibly via gene therapy. The current sequence is that of a canine CC immunoglobulin light chain variable domain framework (FR) peptide of the CC invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 23; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 11 GQPR 14

RESULT 27

ADM07959
ID ADM07959 standard; peptide; 15 AA.

XX AC ADM07959;

XX 20-MAY-2004 (first entry)

PS Claim 3; Page 16; 20pp; English.

CC The present invention relates to complement pathway blocking peptide

CC fragment. The peptide is used to treat a patient suffering from

CC autoimmune disease by blocking the complement pathway, thus preventing

CC immunologic tissue damage, or to treat a patient who is a recipient of a

CC xenograft. The peptide blocks the complement pathway without any tissue

CC damage and disease i.e., without subjecting the patient to an

CC unacceptable risk of the infection

XX Sequence 17 AA;

SQ

Query Match 100.0%; Score 23; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db |||||

8 GQPR 11

RESULT 30

AA49648

ID AAR49648 standard; peptide; 18 AA.

XX AC AAR49648;

XX

DT 25-MAR-2003 (revised)

DT 22-AUG-1994 (first entry)

XX

DE Sequence of peptide for domain 3 of the constant (C) region of the heavy

DE (H) chain (CH3) of an immunoglobulin (Ig).

XX

KW Immunoglobulin; heavy chain; constant region; Camelid.

XX

OS Camelus dromedarius.

XX WO9404678-A1.

PN

PD 03-MAR-1994.

XX

PF 18-AUG-1993; 93WO-EP002214.

XX

PR 21-AUG-1992; 92EP-00402326.

PR 21-MAY-1993; 93EP-00401310.

XX

XX (CAST/) CASTERMAN C.

PA (HAME/) HAMERS R.

XX

XX Casterman C, Hamers R;

XX WPI; 1994-083195/10.

DR

XX Immunoglobulins devoid of light chains - also processes for their

PT preparation, and protein and nucleotide sequence encoding them.

XX

PS Claim 10; Page 61; 87pp; English.

XX

CC A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)

CC polypeptide chains sufficient for the formation of a complete antigen

CC binding site or several such chains. The Ig is devoid of light (L)

CC polypeptide chains. The Ig may be obt. from prokaryotic cells, esp. E.

CC coli, by; cloning a DNA or cDNA sequence coding for the VH domain of an

CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;

CC recovering the cloned fragment after amplification using a 5' primer

CC contg. an Xho site and a 3' primer contg. the Spe site having the

CC sequence in AA04383; cloning the recovered fragment is a vector;

CC transforming host cells; and recovering the expression product of the VHH

CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)

CC region selected from: sequences in AAR49611-16 and AAR49720 for the

CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49622-39 for the CDR3 domain; and/or that its constant region

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

XX Sequence 18 AA;

SQ

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 23; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db |||||

1 GQPR 4

RESULT 31

AA49647

ID AAR49647 standard; peptide; 18 AA.

XX AC AAR49647;

XX

DT 25-MAR-2003 (revised)

DT 22-AUG-1994 (first entry)

XX

DE Sequence of peptide for domain 3 of the constant (C) region of the heavy

DE (H) chain (CH3) of an immunoglobulin (Ig).

XX

KW Immunoglobulin; heavy chain; constant region; Camelid.

XX

OS Camelus dromedarius.

XX WO9404678-A1.

PN

PD 03-MAR-1994.

XX

PF 18-AUG-1993; 93WO-EP002214.

XX

PR 21-AUG-1992; 92EP-00402326.

PR 21-MAY-1993; 93EP-00401310.

XX

XX (CAST/) CASTERMAN C.

PA (HAME/) HAMERS R.

XX

XX Casterman C, Hamers R;

XX WPI; 1994-083195/10.

DR

XX Immunoglobulins devoid of light chains - also processes for their

PT preparation, and protein and nucleotide sequence encoding them.

XX

PS Claim 10; Page 61; 87pp; English.

XX

CC A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)

CC polypeptide chains sufficient for the formation of a complete antigen

CC binding site or several such chains. The Ig is devoid of light (L)

CC polypeptide chains. The Ig may be obt. from prokaryotic cells, esp. E.

CC coli, by; cloning a DNA or cDNA sequence coding for the VH domain of an

CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;

CC recovering the cloned fragment after amplification using a 5' primer

CC contg. an Xho site and a 3' primer contg. the Spe site having the

CC sequence in AA04383; cloning the recovered fragment is a vector;

CC transforming host cells; and recovering the expression product of the VHH

CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)

CC region selected from: sequences in AAR49611-16 and AAR49720 for the

CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49622-39 for the CDR3 domain; and/or that its constant region

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 1 GQPR 4

RESULT 32
 AAR49646
 ID AAR49646 standard; peptide; 18 AA.
 XX AC AAR49646;
 XX DT 25-MAR-2003 (revised)
 DT 22-AUG-1994 (first entry)
 XX DE Sequence of peptide for domain 3 of the constant (C) region of the heavy
 XX (H) chain (CH3) of an immunoglobulin (Ig).
 DE DE
 XX Immunoglobulin; heavy chain; constant region; Camelid.
 XX KW Camelus dromedarius.
 XX OS
 XX PN WO9404678-A1.
 XX PD 03-MAR-1994.
 XX PF 18-AUG-1993; 93WO-EP002214.
 XX PR 21-AUG-1992; 92EP-00402326.
 PR 21-MAY-1993; 93EP-00401310.
 XX (CAST/) CASTERMAN C.
 PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 XX WPI; 1994-083195/10.
 DR Immunoglobulins devoid of light chains - also processes for their
 PT preparation, and protein and nucleotide sequence encoding them.
 XX Claim 10; Page 61; 87pp; English.
 XX A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)
 CC polypeptide chains sufficient for the formation of a complete antigen
 CC binding site or several such chains. The Ig is devoid of light (L)
 CC polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E.
 CC coli, by: cloning a DNA or cDNA sequence coding for the VH domain of an
 CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;
 CC recovering the cloned fragment after amplification using a 5' primer
 CC contg. an Xho site and a 3' primer contg. the Spe site having the
 CC sequence in AA04383; cloning the recovered fragment is a vector;
 CC transforming host cells; and recovering the expression product of the VH
 CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)
 CC region selected from: sequences in AAR49611-16 and AAR49720 for the
 CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or
 CC AAR49622-39 for the CDR3 domain; and/or that its constant region
 CC comprises CH2 and CH3 domains comprising AA sequences selected from, for
 CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that
 CC its hinge region comprises 0-50 AAs, esp. a sequence selected from
 CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 18 AA;
 QY Query Match 100.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 GQPR 4
 ||||

Db 1 GQPR 4

RESULT 33
 AAR49534
 ID AAR49534 standard; peptide; 18 AA.
 XX AC AAR49534;
 XX DT 25-MAR-2003 (revised)
 DT 04-SEP-1994 (first entry)
 XX DE Human Ig heavy chain constant region CH3 gamma-4.
 XX Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
 KW IgG2; IgG3.
 XX OS Homo sapiens.
 XX PN EP584421-A1.
 XX PD 02-MAR-1994.
 XX PF 21-AUG-1992; 92EP-00402326.
 PR 21-AUG-1992; 92EP-00402326.
 XX (CAST/) CASTERMAN C.
 PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 XX WPI; 1994-067061/09.
 DR New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obtd. from Camelid serum,
 PT for use as antibodies.
 XX Disclosure; Page 22; 35pp; English.
 XX This Ig heavy chain constant region CH3 gamma-4 sequence corresponds to
 CC the equivalent gamma-3 sequence (AAR49531) of a camel 2-chain Ig molecule
 CC (100 kDa) which lacks any light chains. The Ig has e.g. improved
 CC solubility and aggregate much less than heavy chains of 4-chain Igs. The
 CC Igs can be used normally for e.g. diagnosis, therapy, in vaccines, for
 CC isolation and purification of antigens and in the production of anti-
 CC idiotypic antibodies. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 18 AA;
 QY Query Match 100.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 GQPR 4
 ||||
 Db 1 GQPR 4

RESULT 34
 AAR49533
 ID AAR49533 standard; peptide; 18 AA.
 XX AC AAR49533;
 XX DT 25-MAR-2003 (revised)
 DT 04-SEP-1994 (first entry)
 XX DE Human Ig heavy chain constant region CH3 gamma-2/gamma-3.
 XX Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
 KW IgG2; IgG3.
 XX

OS Homo sapiens.
 XX EP584421-A1.
 XX
 XX PD 02-MAR-1994.
 XX
 XX PF 21-AUG-1992; 92EP-00402326.
 XX PR 21-AUG-1992; 92EP-00402326.
 XX PA (CAST/) CASTERMAN C.
 XX PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 XX PI WPI; 1994-067061/09.
 XX
 XX PT New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obtd. from Camelid serum,
 PT for use as antibodies.
 XX PS Disclosure; Page 22; 35pp; English.
 XX
 XX CC This Ig heavy chain constant region CH3 gamma-2/gamma-3 sequence
 CC corresponds to the equivalent gamma-3 sequence (AAR49531) of a camel 2-
 CC chain Ig molecule (100 kDa) which lacks any light chains. The Ig has e.g.
 CC improved solubility and aggregate much less than heavy chains of 4-chain
 CC IgG. The IgG can be used normally for e.g. diagnosis, therapy, in
 CC vaccines, for isolation and purification of antigens and in the
 CC production of anti-idiotypic antibodies. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 23; DB 2; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GQPR 4
 XX DB ||||
 XX 1 GQPR 4
 XX
 XX RESULT 35
 XX AAR49532
 XX ID AAR49532 standard; peptide; 18 AA.
 XX
 XX AC AAR49532;
 XX
 XX DT 25-MAR-2003 (revised)
 XX DT 04-SEP-1994 (first entry)
 XX
 XX DE Human Ig heavy chain constant region CH3 gamma-1.
 XX
 XX KW Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
 XX IgG2; IgG3.
 XX
 XX OS Homo sapiens.
 XX
 XX XX EP584421-A1.
 XX
 XX PD 02-MAR-1994.
 XX
 XX PF 21-AUG-1992; 92EP-00402326.
 XX PR 21-AUG-1992; 92EP-00402326.
 XX PA (CAST/) CASTERMAN C.
 XX PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 XX PI WPI; 1994-067061/09.
 XX
 XX PT New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obtd. from Camelid serum,
 PT for use as antibodies.
 XX PS Disclosure; Page 22; 35pp; English.
 XX
 XX CC This Ig heavy chain constant region CH3 gamma-2/gamma-3 sequence
 CC corresponds to the equivalent gamma-3 sequence (AAR49531) of a camel 2-
 CC chain Ig molecule (100 kDa) which lacks any light chains. The Ig has e.g.
 CC improved solubility and aggregate much less than heavy chains of 4-chain
 CC IgG. The IgG can be used normally for e.g. diagnosis, therapy, in
 CC vaccines, for isolation and purification of antigens and in the
 CC production of anti-idiotypic antibodies. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 23; DB 2; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GQPR 4
 XX DB ||||
 XX 1 GQPR 4
 XX
 XX RESULT 35
 XX AAR49532
 XX ID AAR49532 standard; peptide; 18 AA.
 XX
 XX AC AAR49532;
 XX
 XX DT 25-MAR-2003 (revised)
 XX DT 04-SEP-1994 (first entry)
 XX
 XX DE Human Ig heavy chain constant region CH3 gamma-1.
 XX
 XX KW Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
 XX IgG2; IgG3.
 XX
 XX OS Homo sapiens.
 XX
 XX XX EP584421-A1.
 XX
 XX PD 02-MAR-1994.
 XX
 XX PF 21-AUG-1992; 92EP-00402326.
 XX PR 21-AUG-1992; 92EP-00402326.
 XX PA (CAST/) CASTERMAN C.
 XX PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 XX PI WPI; 1994-067061/09.
 XX
 XX PT New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obtd. from Camelid serum,
 PT for use as antibodies.
 XX PS Disclosure; Page 22; 35pp; English.
 XX
 XX CC This Ig heavy chain constant region CH3 gamma-1 sequence corresponds to
 CC the equivalent gamma-3 sequence (AAR49531) of a camel 2-chain Ig molecule
 CC (100 kDa) which lacks any light chains. The Ig has e.g. improved
 CC solubility and aggregate much less than heavy chains of 4-chain IgG. The
 CC IgG can be used normally for e.g. diagnosis, therapy, in vaccines, for
 CC isolation and purification of antigens and in the production of anti-
 CC idiotypic antibodies. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 23; DB 2; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GQPR 4
 XX DB ||||
 XX 1 GQPR 4
 XX
 XX RESULT 36
 XX ABR57545
 XX ID ABR57545 standard; peptide; 22 AA.
 XX
 XX AC ABR57545;
 XX
 XX DT 04-AUG-2003 (first entry)
 XX
 XX DE Anti-angiogenic peptide RAND1.
 XX
 XX KW Cytostatic; Neuropilin-1 receptor; NP-1 receptor; angiogenesis; cancer;
 XX Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PIGF; VEGF;
 XX Placental Growth Factor; Vascular Endothelial Growth Factor;
 XX anti-angiogenic.
 XX
 XX OS Unidentified.
 XX
 XX PN WO2003029275-A2.
 XX
 XX PD 10-APR-2003.
 XX
 XX PF 02-OCT-2002; 2002WO-US031386.
 XX
 XX PR 03-OCT-2001; 2001US-0326712P.
 XX
 XX PA (REG-) REGENERON PHARM INC.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX
 XX PI Rosenbaum JS, Jones DR, Whitaker GB;
 XX WPI; 2003-371982/35.
 XX
 XX PT New anti-angiogenic peptides that are capable of binding to NP-1 or
 XX PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,
 XX PT useful for treating diseases characterized by abnormal angiogenesis, such
 XX PT as cancer.
 XX
 XX PS Disclosure; Page 113; 115pp; English.
 XX
 XX CC The present invention relates to peptides that are capable of binding to
 XX CC Neuropilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor
 XX CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a
 XX CC combination of peptides from Exon 6 of Placental Growth Factor (PIGF),
 XX CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial
 XX CC Growth Factor (VEGF) isoform 165 (VEGF165), also referred to as P6V8) or
 XX CC Exon 7 of PIGF (referred to as P6P7). The peptides and compositions are
 XX CC useful for treating diseases characterised by abnormal angiogenesis, such

CC as cancer. The present peptide is an anti-angiogenic peptide used to
 CC illustrate the invention

SQ Sequence 22 AA;

Query Match 100.0%; Score 23; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 8 GQPR 11

RESULT 37

AAP30407
 ID AAP30407 standard; peptide; 23 AA.

XX AC AAP30407;

DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)

XX DE Sequence of residues 335-357 of immunoglobulin G (IgG).

XX DE DE Sequence of residues 335-357 of immunoglobulin G (IgG).

XX KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.

XX OS Synthetic.

XX PN EP94233-A.

XX PD 16-NOV-1983.

XX PF 09-MAY-1983; 83EP-00302601.

XX PR 11-MAY-1982; 82US-00377223.

XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.

XX PI Weigle WO, Morgan EL;

XX DR WPI; 1983-822296/47.

XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 response in treating cancers, infections etc.

XX PS Disclosure; Page 20; 54pp; English.

XX CC The inventors claim cpds. which include the 23 amino acid sequence
 represented by residues 335-357 of IGG to which is bonded, by amide
 formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 dehydration of homoserine. The cpds. are useful for treating cancers,
 parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 7 GQPR 10

RESULT 38

AAP30405

ID AAP30405 standard; peptide; 23 AA.

XX AC AAP30405;

DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)

XX DE Sequence of residues 335-357 of immunoglobulin G (IgG).

XX KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.

XX OS Synthetic.

XX PN EP94233-A.

XX PD 16-NOV-1983.

XX PF 09-MAY-1983; 83EP-00302601.

XX PR 11-MAY-1982; 82US-00377223.

XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.

XX PI Weigle WO, Morgan EL;

XX DR WPI; 1983-822296/47.

XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 response in treating cancers, infections etc.

XX PS Disclosure; Page 20; 54pp; English.

XX CC The inventors claim cpds. which include the 23 amino acid sequence
 represented by residues 335-357 of IGG to which is bonded, by amide
 formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 dehydration of homoserine. The cpds. are useful for treating cancers,
 parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 7 GQPR 10

RESULT 39

AAP30404

ID AAP30404 standard; peptide; 23 AA.

XX AC AAP30404;

DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)

XX DE Sequence of residues 335-357 of immunoglobulin G (IgG).

XX KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.

XX OS Synthetic.

XX PN EP94233-A.

XX PD 16-NOV-1983.
 XX XX
 XX PF 09-MAY-1983; 83EP-00302601.
 XX XX
 XX PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WFI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.
 XX XX
 CC CC The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 XX SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB ||||
 7 GQPR 10
 RESULT 41
 AAP30409
 ID AAP30409 standard; peptide; 23 AA.
 XX XX
 AC AAP30409;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX XX
 DE Sequence of residues 335-357 of immunoglobulin G (IGG).
 XX XX
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 KW natural killer cell.
 XX XX
 OS Synthetic.
 XX XX
 FN EP94233-A.
 XX XX
 PD 16-NOV-1983.
 XX XX
 PF 09-MAY-1983; 83EP-00302601.
 XX XX
 PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WFI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.
 XX XX
 CC CC The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 XX SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 DB ||||
 7 GQPR 10
 RESULT 40
 AAP30406
 ID AAP30406 standard; peptide; 23 AA.
 XX XX
 AC AAP30406;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX XX
 DE Sequence of residues 335-357 of immunoglobulin G (IGG).
 XX XX
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 KW natural killer cell.
 XX XX
 OS Synthetic.
 XX XX
 FN EP94233-A.
 XX XX
 PD 16-NOV-1983.
 XX XX
 PF 09-MAY-1983; 83EP-00302601.
 XX XX
 PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WFI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB ||||
 7 GQPR 10

RESULT 42
 ADH89371 ID ADH89371 standard; peptide; 23 AA.
 XX AC ADH89371;
 XX DT 15-APR-2004 (first entry)
 XX DE Human transferrin fusion protein-related peptide SeqID15.
 XX KW fusion protein; transferrin protein; glycosylation;
 KW antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection; human.
 XX OS Homo sapiens.
 XX PN US2003226155-A1.
 XX PD 04-DEC-2003.
 XX PF 10-MAR-2003; 2003US-00384060.
 XX PR 30-AUG-2001; 2001US-0315745P.
 XX PR 30-NOV-2001; 2001US-0334059P.
 XX PR 30-AUG-2002; 2002US-0023149P.
 XX PR 30-AUG-2002; 2002US-0406977P.
 XX PA (BIOR-) BIOREXIS PHARM CORP.
 XX PI Sadeghi H, Prior CP, Turner A;
 XX WPI; 2004-022093/02.
 XX PT New fusion protein comprising a transferrin protein exhibiting reduced
 PT glycosylation fused to at least one antibody variable region, useful for
 PT preparing a composition for treating e.g., septic shock, neoplasm or
 PT autoimmune disease.
 XX PS Disclosure; SEQ ID NO 15; 82pp; English.
 XX CC This invention relates to a novel fusion protein which comprises a
 CC transferrin protein exhibiting reduced glycosylation fused to at least
 CC one antibody variable region. The invention may be useful for the
 CC development of compounds with cytostatic, antibacterial, virucide,
 CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
 CC the sequences disclosed may be useful for gene therapy. The fusion
 CC protein is useful for preparing a composition for treating a disease or
 CC disease symptom in a patient for example septic shock, endotoxin shock,
 CC cachexia syndromes associated with bacterial, viral or parasitic
 CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
 CC associated with treatment for preventing graft rejection. The present
 CC sequence is that of a peptide which is related to the invention.
 XX Sequence 23 AA;
 QY Query Match 100.0%; Score 23; DB 8; Length 23;
 DB Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB ||||
 7 GQPR 10

RESULT 43
 ADS97551 ID ADS97551 standard; protein; 23 AA.
 XX AC ADS97551;
 XX DT 16-DEC-2004 (first entry)
 XX DE Dementia related secretogranin 1 peptide DRES-17.
 XX KW DRES-17; dementia related secretogranin 1; secretogranin 1;
 KW Alzheimer's disease; diagnosis; gene therapy; human; marker.
 XX OS Homo sapiens.
 XX PN WO2004082455-A2.
 XX PD 30-SEP-2004.
 XX PF 18-MAR-2004; 2004WO-BP002824.
 XX PR 18-MAR-2003; 2003EP-00005968.
 XX PR 07-JAN-2004; 2004EP-00000170.
 XX PA (BIOV-) BIOVISION AG.
 XX PI Lamping N, Zucht H, Selle H, Juergens M, Heine G, Hess R;
 XX PI Kellmann M, Lamerz J, Moehring T;
 XX WPI; 2004-718701/70.
 XX PT Detecting a neurological disease, particularly Alzheimer's disease,
 PT comprises determining at least one dementia related secretogranin 1
 PT (DRES) peptide, or at least one peptide corresponding to GeneBank
 PT Accession No NM001819.
 XX PS Claim 1; SEQ ID NO 17; 110pp; English.
 XX CC The present sequence is that of dementia related secretogranin 1 peptide
 CC DRES-17 (mass 2522.1 Da), corresponding to amino acids 253-275 of human
 CC secretogranin 1 ADS97579. The peptide can be used as a marker in claimed
 CC methods of the invention for detecting a neurological disease, preferably
 CC Alzheimer's disease (AD), or a predisposition to such a disease.
 CC Detection of AD is based on the finding that the concentration of certain
 CC peptides is changed in bodily fluid samples, especially in the
 CC cerebrospinal fluid, of AD patients relative to their concentration in
 CC control samples. A method for detecting a neurological disease, in
 CC particular a chronic dementia disease, especially AD or a predisposition
 CC to such a disease involves the detection of at least one DRES peptide
 CC ADS97535-ADS97578 and ADS97581-ADS97591 in a biological sample.
 CC Preferably, the peptide(s) is determined in combination with one or more
 CC peptides derived from chromogranin A ADS97606-ADS97619, secretogranin 2
 CC ADS97595-ADS97605 and/or secretogranin 5 ADS97592-ADS97594. The disease
 CC can be detected at an early stage e.g. in the diagnosis of mild cognitive
 CC impairment, or in neurological diseases other than AD, such as Lewy body
 CC dementia, vascular dementia or depression. Determination of the marker
 CC peptides is conducted by an activity, immunological, molecular
 CC biological, physical or chemical assay. Preferably the mass of the
 CC peptide is determined by mass spectrometry. Pharmaceutical products
 CC comprise the marker peptides, antibodies directed to the peptides,
 CC nucleic acids corresponding to the peptides, a ribozyme, antisense
 CC nucleic acid, triplex-forming nucleic acid or RNAi nucleic acid, peptide
 CC antagonists or peptide agonists for the therapy, diagnosis, prognosis or
 CC prophylaxis of neurological diseases, particularly AD. The marker
 CC peptides may be mutated at 1 or 2 amino acid positions corresponding to
 CC the non-mutated DRES sequence, or chemically or enzymatically modified,
 CC or post-translationally modified, preferably phosphorylated, sulfated,
 CC oxidised or C-terminally amidated, or have a pyroglutamate modification
 CC in an individual's biological sample.
 XX Sequence 23 AA;
 QY

RESULT 45	
AAU89298	
ID ID	AAU89298 standard; peptide; 25 AA.
XX AC	AAU89298;
XX DT	18-JUN-2002 (first entry)
XX XX	Insulin/insulin-like growth factor receptor-binding peptide #1354.
DE DE	
XX XX	Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW KW	ophthalmological; insulin; receptor; gene therapy; diabetes;
KW KW	insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW KW	diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX OS	Synthetic.
XX XX	
PN PN	WO200172771-A2.
XX XX	04-OCT-2001.
XX PF	29-MAR-2000; 2000WO-US008528.
XX PR	29-MAR-2000; 2000WO-US008528.
XX XX	(DGIB-) DGI BIOTECHNOLOGIES LLC.
PA PA	(NOVO) NOVO NORDISK AS.
XX XX	
PI PI	Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI PI	Brisette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
PI PI	Hansen PH, Ravera M, Hsiao K;
XX DR	WPI; 2002-025774/03.
XX XX	
PT PT	Modulating insulin activity in mammalian cells, for treating e.g.
PT PT	diabetes and tumors, comprises using peptides that bind to insulin or
PT PT	insulin-like growth factor receptors.
XX XX	
PS PS	Disclosure; Fig 2E; 390pp; English.
XX CC	
CC CC	The invention relates to a method of modulating insulin activity in
CC CC	mammalian cells by administering a peptide that binds the insulin
CC CC	receptor (IR). A composition containing a peptide, optionally expressed
CC CC	from gene therapy vectors, that binds to site 1 of IR and an insulin
CC CC	agonist are useful for treating diabetes. Also, peptides that are
CC CC	antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC CC	useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC CC	(e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC CC	receptor agonists are useful for treating neurological diseases,
CC CC	including stroke and diabetic neuropathy. The peptides are also useful in
CC CC	screening for compounds that bind to IR or IGF-1 receptor, potential
CC CC	therapeutics and research reagents. AAU89334-AAU90957 represent IR and/or
CC CC	IGF-1 receptor-binding peptides and related amino acid sequences of the
XX CC	invention
XX XX	
SQ	Sequence 25 AA;
Query Match	100.0%; Score 23; DB 5; Length 25;
Best Local Similarity	100.0%; Pred. No. 5.5e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GQPR 4
Db	12 GQPR 15
RESULT 46	
ABO23580	
ID ID	ABO23580 standard; protein; 27 AA.
XX AC	
XX AC	ABO23580;
XX XX	

DT 04-SEP-2003 (first entry)
 XX Mycobacterium tuberculosis outlier protein #6.
 DE
 XX
 XX Candidate protein identification; pathogen; anti-infective;
 KW outlier protein; virulence protein; antigen; drug target protein;
 KW pathogenic organism; antimicrobial.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX US2003039963-A1.
 PN 27-FEB-2003.
 XX
 XX 30-MAR-2001; 2001US-00820843.
 PF 30-MAR-2001; 2001US-00820843.
 XX
 XX (BRAH/) BRAHMACHARI S K.
 PA (RAMA/) RAMACHANDRAN S.
 PA (NAND/) NANDI T.
 PA (BHIM/) BHIMARAO C.
 XX
 XX Brahmachari SK, Ramachandran S, Nandi T, Bhimmarao C;
 PI WPI; 2003-492159/46.
 XX
 XX Identifying candidate proteins useful as anti-infectives involves
 PT matching outlier protein sequences with protein sequences in databases.
 PT
 XX
 XX Example 7; Page 80; 117pp; English.
 XX
 XX The present invention relates to a method for identifying candidate
 CC proteins in pathogens useful as anti-infectives. The invention discloses
 CC a computational method which involves the calculation of several sequence
 CC attributes and their subsequent analysis results in the identification
 CC of outlier proteins in different pathogens. The method is useful for the
 CC identification of outlier proteins (e.g. virulence proteins, antigens or
 CC proteins used as drug targets) in pathogenic organisms. The method of the
 CC invention provides reproducible results as it does not depend on the
 CC variable biochemical characterisation of proteins. ABO23500-ABO23617
 CC represent outlier proteins identified from different pathogenic organisms
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 23; DB 7; Length 27;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 2 GQPR 5
 RESULT 47
 AAW37936
 ID AAW37936 standard; peptide; 28 AA.
 AC
 XX
 XX AAW37936;
 XX
 XX 27-AUG-2003 (revised)
 DT 10-AUG-1998 (first entry)
 XX
 XX Herpes virus detection peptide.
 DE
 XX
 XX Herpes virus detection peptide; Kasopi's sarcoma-associated Herpes virus;
 KW vaccine; Herpes Simplex Virus I; Herpes Virus II; Human Cytomegalovirus;
 KW Varicella Zoster Virus; Marek's Disease Virus; Epstein Barr Virus;
 KW Herpes Virus IV.
 XX
 XX Synthetic.
 OS
 OS Human herpesvirus 8.
 XX

PN US5760175-A.
 XX
 PD 02-JUN-1998.
 XX
 PF 05-SEP-1996; 96US-00708893.
 XX
 PR 05-SEP-1996; 96US-00708893.
 XX
 PA (BIOV-) BIO-VIRUS RES INC.
 XX
 PI Golubev DB, Chaihorsky A;
 XX
 DR WPI; 1998-332242/29.
 XX
 PT New peptide homologous to Kasopi's Sarcoma-Associated Herpes Virus sub-
 PT units - is useful for the detection of, and vaccination against several
 PT herpes virus infections.
 XX
 PS Claim 1; Col 5-6; 4pp; English.
 XX
 CC This is the amino acid sequence of the novel Herpes virus detection
 CC peptide, which is homologous with the parts of the subunits of the
 CC Kasopi's sarcoma-associated Herpes virus. It is useful for use as a
 CC vaccine against pathogenic development of several herpes infections, e.g.
 CC Herpes Simplex Virus I and II, Human Cytomegalovirus, Varicella Zoster
 CC Virus, Marek's Disease Virus, Epstein Barr Virus and especially Kasopi's
 CC Sarcoma-Associated Herpes Virus. The peptide is also useful for the
 CC detection of herpes type-4 virus. (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 23; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 24 GQPR 27
 RESULT 48
 AAY56879
 ID AAY56879 standard; peptide; 28 AA.
 AC
 XX
 XX AAY56879;
 XX
 DT 12-SEP-2003 (revised)
 DT 14-APR-2000 (first entry)
 XX
 XX Peptide in a vaccine against Kasopi's sarcoma-associated herpes virus.
 DE
 XX
 XX Immune response; herpes virus; vaccine.
 KW
 XX Human herpesvirus 8.
 OS
 XX US6015566-A.
 PN
 PD 18-JAN-2000.
 XX
 XX 01-JUN-1998; 98US-00088154.
 PF
 XX
 PR 05-SEP-1996; 96US-00708893.
 XX
 PA (BIOV-) BIO-VIRUS RES INC.
 XX
 PI Golubev DB, Chaihorsky A;
 XX
 DR WPI; 2000-126310/11.
 XX
 XX Vaccine against herpes viruses, especially Kasopi's sarcoma-associated
 PT herpes virus, comprises specific peptide coupled to carrier protein.
 XX

PS Disclosure; Col 2; 5pp; English.

XX The invention provides a composition for generating an immune response to

CC a herpes virus. The composition comprises the present sequence conjugated

CC to a carrier is useful as a vaccine against various herpes viruses,

CC especially Kaposi's sarcoma-associated herpes virus. (Updated on 12-SEP-

CC 2003 to standardise OS field)

XX

SQ Sequence 28 AA;

Query Match 100.0%; Score 23; DB 3; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4

Db 24 GQPR 27

RESULT 49

ABO54482

ID ABO54482 standard; protein; 31 AA.

XX

AC ABO54482;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human genome derived single exon protein #716.

XX

KW Human; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX

OS Homo sapiens.

XX

PN US2003194704-A1.

XX

PD 16-OCT-2003.

XX

PF 03-APR-2002; 2002US-00029386.

XX

PR 03-APR-2002; 2002US-00029386.

XX

PA (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX

PI Penn SG, Rank DR, Hanzel DK;

XX

DR WPI; 2004-119264/12.

XX

PT New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX

PS Claim 45; SEQ ID NO 28116; 80pp; English.

XX

CC The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterising

CC alternative splicing events, in detecting and characterising gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe protein of the invention. Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 23; DB 8; Length 31;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4

Db 28 GQPR 31

RESULT 50

AAB51356

ID AAB51356 standard; peptide; 33 AA.

XX

AC AAB51356;

XX

DT 09-APR-2001 (first entry)

XX

DE Mouse blood cell growth inhibiting factor related peptide SEQ ID NO:2.

XX

KW Mouse; blood cell growth inhibiting factor; BGIF; proliferation;

KW lymph-haematopoietic cell; lymph-haematopoietic system disease;

KW diagnosis.

XX

OS Mus musculus.

XX

PN JP2000300264-A.

XX

PD 31-OCT-2000.

XX

PF 14-APR-1999; 99JP-00107246.

XX

PR 14-APR-1999; 99JP-00107246.

XX

PS (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.

XX

DR WPI; 2001-141349/15.

XX

PT A protein with growth inhibiting activity to lymph-hematopoietic cells,

PT useful for the diagnosis and treatment of lymph-hematopoietic system

PT diseases.

XX

PS Example 2; Page 15; 21pp; Japanese.

XX

CC The present invention describes a mouse blood cell growth-inhibiting

CC factor (BGIF) protein derived from BMS (bone marrow stem cells) 2.4 cells

CC having inhibitory activity to the growth of lymph-haematopoietic cells.

CC The BGIF gene and protein are useful for the diagnosis and treatment of

CC lymph-haematopoietic system diseases. The present sequence represents an

CC amino acid sequence which is used in an example from the present

CC invention

XX

SQ Sequence 33 AA;
 Query Match 100.0%; Score 23; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 13 GQPR 16
 RESULT 51
 AAY19644
 ID AAY19644 standard; protein; 35 AA.
 XX AC AAY19644;
 XX DT 14-JUL-1999 (first entry)
 XX DE SEQ ID NO 362 from WO9922243.
 XX KW Human secreted protein; cancer; tumour; neurodegenerative disorder;
 KW developmental abnormality; fetal deficiency; blood disorder; leukemia;
 KW immune system disease; autoimmune disease; hepatic disease;
 KW renal disease; lymphoma; inflammation; allergy; ischemic shock;
 KW Alzheimer's; cognitive disorder; schizophrenia; prostate disease;
 KW obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;
 KW lung disease; thymus disease; digestive disorder; endocrine disorder;
 KW infection; AIDS.
 XX OS Homo sapiens.
 XX PN WO9922243-A1.
 XX PD 06-MAY-1999.
 XX XX 23-OCT-1998; 98WO-US022376.
 XX PR 24-OCT-1997; 97US-0062784P.
 XX PR 24-OCT-1997; 97US-0063088P.
 XX PR 24-OCT-1997; 97US-0063089P.
 XX PR 24-OCT-1997; 97US-0063090P.
 XX PR 24-OCT-1997; 97US-0063091P.
 XX PR 24-OCT-1997; 97US-0063092P.
 XX PR 24-OCT-1997; 97US-0063097P.
 XX PR 24-OCT-1997; 97US-0063098P.
 XX PR 24-OCT-1997; 97US-0063099P.
 XX PR 24-OCT-1997; 97US-0063100P.
 XX PR 24-OCT-1997; 97US-0063101P.
 XX PR 24-OCT-1997; 97US-0063109P.
 XX PR 24-OCT-1997; 97US-0063110P.
 XX PR 24-OCT-1997; 97US-0063111P.
 XX PR 24-OCT-1997; 97US-0063148P.
 XX PR 24-OCT-1997; 97US-0063386P.
 XX PR 24-OCT-1997; 97US-0063387P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Feng P, Rosen CA, Ruben SM, Ni J, Wei Y, Soppet DR, Moore PA;
 PI Kayw H, Latleur DW, Olsen HS, Brewer LA, Shi Y, Ebner R, Young P;
 PI Greene JM, Florence KA, Florence C, Duan DR, Janat F, Endress GA;
 PI Carter KC;
 XX WPI; 1999-303069/25.
 XX PT New isolated human genes and the secreted polypeptides they encode.
 XX PS Disclosure; Page 482; 546pp; English.
 XX CC The specification describes human secreted proteins. The polynucleotides
 CC and their corresponding secreted polypeptides are useful for preventing,
 CC treating or ameliorating medical conditions, e.g. by protein or gene
 CC therapy. Pathological conditions can also be diagnosed by determining the

CC amount of the polypeptides in a sample or by determining the presence of
 CC mutations in the polynucleotides. Specific uses are described for each of
 CC the polynucleotides, based on which tissues they are most highly
 CC expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, neurodegenerative disorders, developmental
 CC abnormalities and fetal deficiencies, blood disorders, leukemias,
 CC diseases of the immune system, autoimmune diseases, hepatic and renal
 CC disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, prostate diseases, obesity,
 CC disorders involving osteoclasts such as osteoporosis, arthritis or
 CC malignancies, diseases of testes, lung or thymus, digestive/endocrine
 CC disorders, infections and AIDS. The polypeptides are also useful for
 CC identifying their binding partners
 XX Sequence 35 AA;
 SQ Query Match 100.0%; Score 23; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 3 GQPR 6
 RESULT 52
 AAY98355
 ID AAY98355 standard; peptide; 35 AA.
 XX AC AAY98355;
 XX DT 31-JUL-2000 (first entry)
 XX DE Alpha D peptide derived from TrkC SEQ ID NO:70.
 XX KW Alpha D peptide; Alpha D region; protein kinase; modulation; activity;
 KW cytosolic; anti-diabetic; anorectic; antiinflammatory; dermatological;
 KW immunosuppressive; immunomodulator; osteopathic; cardiant; vasotropic;
 KW antiarteriosclerotic; protein kinase modulator; cancer; proliferation;
 KW restenosis; atherosclerosis; skin disorder; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder; osteoporosis;
 KW autoimmune disease; immune disorder; cardiovascular disease.
 XX OS Homo sapiens.
 XX PN WO200018895-A1.
 XX PD 06-APR-2000.
 XX PR 24-SEP-1999; 99WO-US022106.
 XX PR 25-SEP-1998; 98US-00161094.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX PI Ben-Sasson SA;
 XX WPI; 2000-328722/28.
 XX PT Peptide derivatives of protein kinase alpha D regions which selectively
 XX modulate the activity of protein kinases.
 XX PS Claim 53; Fig 1; 148pp; English.
 XX CC The present invention describes a peptide derivative (A) of the protein
 CC kinase alpha D region comprising 5-30 amino acids, which modulates the
 CC activity of the protein kinase. AAY98286 to AAY98455 represent peptides
 CC derived from protein kinase alpha D regions, which are used in the
 CC exemplification of the present invention. The peptides have cytostatic,
 CC anti-diabetic, anorectic, antiinflammatory, dermatological, cardiant,
 CC immunosuppressive, immunomodulator, osteopathic, vasotropic and
 CC antiarteriosclerotic activities, and are protein kinase modulators. The

CC peptides can be used as test peptides to identify protein kinase
 CC modulators. They can also be used to modulate the activity of a protein
 CC kinase in a subject, and in a method of detecting a ligand that binds to
 CC the alpha D region of a protein kinase. They may be used to produce
 CC antibodies that bind to the alpha D region of a protein kinase. The
 CC peptides are useful in the treatment of diseases caused by over- or under
 CC -activity of a protein kinase, e.g. cancer, diseases caused by
 CC proliferation of smooth muscle (e.g. restenosis and atherosclerosis),
 CC skin disorders, diabetes, obesity, diseases of the central nervous
 CC system, inflammatory disorders, autoimmune diseases and other immune
 CC disorders, osteoporosis and cardiovascular diseases
 XX
 SQ Sequence 35 AA;

Query Match 100.0%; Score 23; DB 3; Length 35;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 26 GQPR 29

RESULT 53

AAW82815

ID AAW82815 standard; protein; 35 AA.

AC AAW82815;

XX

XX

DT 07-NOV-2001 (first entry)

XX

XX

DE Human immune/haematopoietic antigen SEQ ID NO:10408.

XX

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW Cytostatic; gene therapy; vaccine; metastasis.

XX

OS Homo sapiens.

XX

XX

PN WO200157182-A2.

XX

XX

PD 09-AUG-2001.

XX

XX

PF 17-JAN-2001; 2001WO-US001354.

XX

XX

PR 31-JAN-2000; 2000US-0179065P.

PR

PR 04-FEB-2000; 2000US-0180628P.

PR

PR 24-FEB-2000; 2000US-0184664P.

PR

PR 02-MAR-2000; 2000US-0186350P.

PR

PR 16-MAR-2000; 2000US-0189874P.

PR

PR 17-MAR-2000; 2000US-0190076P.

PR

PR 18-APR-2000; 2000US-0198123P.

PR

PR 19-MAY-2000; 2000US-0205515P.

PR

PR 07-JUN-2000; 2000US-0209467P.

PR

PR 28-JUN-2000; 2000US-0214886P.

PR

PR 30-JUN-2000; 2000US-0215135P.

PR

PR 07-JUL-2000; 2000US-0216647P.

PR

PR 07-JUL-2000; 2000US-0216880P.

PR

PR 11-JUL-2000; 2000US-0217487P.

PR

PR 11-JUL-2000; 2000US-0217496P.

PR

PR 14-JUL-2000; 2000US-0218290P.

PR

PR 26-JUL-2000; 2000US-0220963P.

PR

PR 26-JUL-2000; 2000US-0220964P.

PR

PR 14-AUG-2000; 2000US-0224518P.

PR

PR 14-AUG-2000; 2000US-0224519P.

PR

PR 14-AUG-2000; 2000US-0225213P.

PR

PR 14-AUG-2000; 2000US-0225214P.

PR

PR 14-AUG-2000; 2000US-0225266P.

PR

PR 14-AUG-2000; 2000US-0225267P.

PR

PR 14-AUG-2000; 2000US-0225268P.

PR

PR 14-AUG-2000; 2000US-0225270P.

PR

PR 14-AUG-2000; 2000US-0225447P.

PR

PR 14-AUG-2000; 2000US-0225757P.

PR

PR 14-AUG-2000; 2000US-0225758P.

PR

PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 13-OCT-2000; 2000US-0239337P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 08-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 DR N-PSDB; AAK55596.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX Claim 11; SEQ ID NO 10408; 3071pp + Sequence Listing; English.
 PS AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK34942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 35 AA;
 SQ Query Match 100.0%; Score 23; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 ||||

Db 22 GQPR 25

RESULT 54
 AAU83474
 ID AAU83474 standard; peptide; 35 AA.
 XX AAU83474;
 AC AAU83474;
 XX 08-MAY-2002 (first entry)
 DT Human phospholipase A2 X peptide #1.
 DE XX
 DE XX
 KW Phospholipase A2; enzyme; PLA2; virucide; antirheumatic; antiarthritic;
 KW immunosuppressive; parvovirus; Vllup; gene therapy;
 KW viral-associated disease; rheumatoid arthritis; systemic erythematosis;
 KW adult-onset Still's disease; polyarthritis.
 XX OS Homo sapiens.
 XX WO200200924-A2.
 PN 03-JAN-2002.
 PD 28-JUN-2001; 2001WO-CA000932.
 PF 28-JUN-2000; 2000CA-02310263.
 PR (NARE-) INST NAT RECH SCI.
 XX Tijssen P, Zadori Z;
 XX WPI; 2002-139932/18.
 XX New viral phospholipase A2 enzymes, useful in gene therapy for treating a
 PT subject viral-associated disease, e.g. rheumatoid arthritis, systemic
 PT erythematosis, adult-onset Still's disease or polyarthritis.
 XX Example 1; Fig 2; 107pp; English.
 XX The invention relates to an isolated viral polypeptide having
 CC phospholipase A2 (PLA2) activity (e.g. Vllup from parvovirus) and the
 CC polynucleotides encoding them. Also included are a peptide that
 CC specifically binds a viral phospholipase A2 being (WY)-(CIVL)-G-X-(GP)-
 CC (GKNS)-x(8,14)-D-x(2)-(AC)-x(2)-x(2)-H-D-x(2)-Y. () = indicates the
 CC presence of one of the enclosed amino acids at this position; x = any
 CC amino acid; x(2) = a stretch of 2 amino acids; and x(8,14) = a stretch of
 CC 8-14 amino acids or Y-x-G-P-G-x(12)-D-x(2)-A-x(2)-H-D-x(2)-Y, a
 CC polypeptide that is an inactive variant of a viral polypeptide comprising
 CC an amino acid motif as detailed above, an antisense oligonucleotide
 CC complementary to the polynucleotide, a vector comprising the
 CC polynucleotide, a host cell comprising the vector, producing a
 CC recombinant virus comprising genetically engineered viral particles with
 CC the polynucleotide, fragment or vector, an antibody that bind to the
 CC protein, anti viral compounds which inhibit viral phospholipases. The
 CC polynucleotide is useful for gene therapy, and for improving a gene
 CC therapy vector. Where the gene therapy vector is based on an adeno-
 CC associated virus. The antisense oligonucleotide is useful for inhibiting
 CC viral replication and/or infectivity in a subject, for manufacturing a
 CC medicament to treat the infectivity and/or replication of a virus in a
 CC subject or to treat viral-associated disease. The polypeptide is useful
 CC as an in vitro standard for measuring phospholipase A2 activity. The anti
 CC viral agent is used to decrease the infectivity and/or replication of a
 CC virus, e.g. parvovirus, in a subject. The anti-viral agent may also be used
 CC to inhibit a viral phospholipase A2 in a subject in need of such therapy,
 CC where the subject has a viral-associated disease or disorder,
 CC particularly a disease associated with a parvovirus. The viral-associated
 CC disease includes rheumatoid arthritis, systemic erythematosis, adult-
 CC onset Still's disease or polyarthritis. The present sequence is a
 CC phospholipase peptide used to determine the motifs of the invention
 XX Sequence 35 AA;
 SQ

Query Match 100.0%; Score 23; DB 5; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 15 GQPR 18

RESULT 55
 AYW00600
 ID AYW00600 standard; peptide; 36 AA.
 XX
 AC AYW00600;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE BS136 epitope peptide #3.
 XX
 KW Therapy; breast cancer; cytostatic; tumour; metastasis; BS136; EST;
 KW expressed sequence tag; epitope.
 KW
 OS Unidentified.
 XX
 FN US2003104364-A1.
 XX
 XX 05-JUN-2003.
 XX
 PF 25-JUN-1998; 98US-00104750.
 XX
 XX 25-JUN-1997; 97US-00882369.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GRAN/) GRANADOS E N.
 PA (KLAS/) KLAS M R.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 PI Billengel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
 PI Klass MR, Russell JC, Stroupe SD;
 XX
 XX WPI; 2003-801225/75.
 XX
 PT Novel BS136 polypeptide useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating breast diseases such
 PT as breast cancer.
 XX
 XX Claim 7; Page 50; Opp; English.
 XX
 CC The present invention relates to a novel BS136 polypeptide useful for
 CC detecting, diagnosing, preventing and treating breast diseases such as
 CC breast cancer. The invention is useful for preventing action of the
 CC tissue-specific BS136 polypeptide and for the therapeutic treatment of
 CC tumours and metastases. The present sequence is a BS136 epitope peptide
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 23; DB 7; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 19 GQPR 22

RESULT 56
 AAY86343
 ID AAY86343 standard; peptide; 37 AA.
 XX

AC AAY86343;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Human gene 4-encoded protein fragment, SEQ ID NO:258.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9966041-A1.
 PN
 PD 23-DEC-1999.
 XX
 PF 15-JUN-1999; 99WO-US013418.
 XX
 PR 16-JUN-1998; 98US-0089507P.
 PR 16-JUN-1998; 98US-0089508P.
 PR 16-JUN-1998; 98US-0089509P.
 PR 16-JUN-1998; 98US-0089510P.
 PR 22-JUN-1998; 98US-0090112P.
 PR 22-JUN-1998; 98US-0090113P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
 XX
 XX WPI; 2000-106100/09.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 XX Disclosure; Page 12; 586pp; English.
 XX
 CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.,
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 94 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AAY86334 to AAY86585 represent fragments of the secreted proteins
 XX
 SQ Sequence 37 AA;

Query Match 100.0%; Score 23; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 16 GQPR 19

RESULT 57
AB053488
ID AB053488 standard; protein; 37 AA.
XX
AC AB053488;
XX
DT 06-NOV-2003 (first entry)
XX
DE Novel human secreted protein #4 fragment #3.
XX
KW Human; vaccine; immune system disorder; haematopoietic cell disorder;
KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
KW blood platelet disorder; wound; heart attack; myocardial infarction;
KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
KW aberrant cellular division; cell proliferative disorder; angiogenesis;
KW cardiovascular disorder; pulmonary heart disease; neovascularisation;
KW hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; ALS; AIDS;
KW amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
KW cachexia; anorexia; lung damage; infection.
XX
OS Homo sapiens.
XX
PN US2003065151-A1.
XX
PD 03-APR-2003.
XX
PF 04-APR-2002; 2002US-00115123.
XX
PR 16-JUN-1998; 98US-0089507P.
PR 16-JUN-1998; 98US-0089508P.
PR 16-JUN-1998; 98US-0089509P.
PR 16-JUN-1998; 98US-0089510P.
PR 22-JUN-1998; 98US-0090112P.
PR 22-JUN-1998; 98US-0090113P.
PR 15-JUN-1999; 99WO-US013418.
PR 14-DEC-1999; 99US-00461325.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
XX
DR WPI; 2003-531736/50.
XX
PT Novel antibody that binds specifically to a HCEJQ69 protein, useful for
PT detecting the presence of a protein in a biological sample, and for
PT treating cancers, autoimmune disorders and HIV infection.
XX
PS Disclosure; Page 5; 176pp; English.
XX
CC The invention relates to an isolated antibody or its fragment that
CC specifically binds to a protein. The antibody is useful for detecting a
CC protein in a biological sample, by contacting the biological sample with
CC the antibody or its fragment and detecting the protein in the biological
CC sample. The antibody is useful for purifying, detecting and targeting the
CC human secreted proteins, including both in vitro and in vivo diagnostic
CC and therapeutic methods. The antibody is useful for immunophenotyping of
CC cell lines in biological samples and in antibody-based therapies for
CC treating, inhibiting and preventing diseases, disorders or conditions
CC associated with aberrant expression and/or activity of the above
CC proteins. The antibody is useful for treating deficiencies or disorders
CC of immune system and haematopoietic cells, for increasing differentiation
CC and proliferation of haematopoietic cells, for treating immune
CC deficiencies or disorders e.g. cancers, autoimmune disorders (such as
CC rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
CC thrombocytopenia and as a marker for a particular immune system disease
CC or disorder. The antibody is also useful for treating blood coagulation
CC disorders, blood platelet disorders, wounds, heart attacks (infarction),

CC strokes, scarring and asthma. The antibody is also useful for treating or
CC preventing graft-versus host rejection, for modulating inflammation, for
CC treating hyperproliferative disorders e.g. lymphoproliferative disorders
CC and cancers, for inhibiting aberrant cellular division and for treating
CC cell proliferative disorders. The antibody is also useful for treating
CC cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
CC disorders associated with neovascularisation and angiogenesis, for
CC treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
CC retinopathy and uveitis, for wound healing and disorders of epithelial
CC cell proliferation. The antibody is also useful for treating neurological
CC diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
CC increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
CC cachexia and anorexia, for preventing and healing damage to lungs and for
CC treating infectious diseases. The present sequence represents the amino
CC acid sequence of a novel human secreted protein fragment. Note: the
CC specification data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030065151
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 23; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 16 GQPR 19
RESULT 58
AB023432
ID AB023432 standard; peptide; 38 AA.
XX
AC AB023432;
XX
DT 04-SEP-2003 (first entry)
XX
DE Amino acid sequence #72 associated with human secreted proteins.
XX
KW Human; secreted protein; cancer; liver disorder; hepatitis;
KW neural disorder; Alzheimer's disease; cytostatic; neuroprotective;
KW hepatotropic; nootropic.
XX
OS Homo sapiens.
XX
PN US2003050455-A1.
XX
PD 13-MAR-2003.
XX
PF 06-FEB-2001; 2001US-00776724.
XX
PR 16-JUL-1997; 97US-0052661P.
PR 16-JUL-1997; 97US-0052870P.
PR 16-JUL-1997; 97US-0052871P.
PR 16-JUL-1997; 97US-0052872P.
PR 16-JUL-1997; 97US-0052873P.
PR 16-JUL-1997; 97US-0052874P.
PR 16-JUL-1997; 97US-0052875P.
PR 22-JUL-1997; 97US-0053440P.
PR 22-JUL-1997; 97US-0053441P.
PR 22-JUL-1997; 97US-0053442P.
PR 18-AUG-1997; 97US-0056359P.
PR 15-JUL-1998; 98WO-US014613.
PR 14-JAN-1999; 99US-00229982.
PR 08-FEB-2000; 2000US-0180909P.
PR 26-SEP-2000; 2000US-00669688.
XX
(RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.


```

XX WPI: 1992-265591/32.
DR N-PSDB; AAQ26719.
XX
PT Recombinant human hepatocyte growth factor and DNA encoding it - useful
PT for diagnosis and treatment of hepatic disease and transgenic animal
PT prepn.
XX
PS Disclosure; Page 18; 28pp; Japanese.
XX
CC This sequence represents exon VII of human hepatocyte growth factor. See
CC also AAR25676-92, AAQ26713-27
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 23; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 16 GQPR 19

RESULT 61
ID ADP45479 standard; peptide; 40 AA.
XX
AC ADP45479;
XX
XX 09-SEP-2004 (first entry)
XX
DE Human colon cancer cell-associated peptide SeqID202.
XX
XX neoplastic colon cell; cytostatic; vaccine; gene therapy; colon cancer;
XX immune response; metastasis; human.
XX
OS Homo sapiens.
XX
XX WO2004050900-A2.
XX
PD 17-JUN-2004.
XX
XX 04-DEC-2003; 2003WO-US040131.
XX
XX 04-DEC-2002; 2002US-0431143P.
XX
XX 04-DEC-2002; 2002US-0431206P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Turner LR, Sun Y, Rodriguez M;
XX
XX WPI: 2004-480629/45.
XX
XX N-PSDB; ADP45347.
XX
XX Nucleic acid molecules isolated from normal and neoplastic colon cells,
XX useful for treating colon cancer and for identifying, diagnosing,
XX monitoring, staging, and imaging colon cancer and/or non-cancerous
XX disease states in colon.
XX
XX Claim 12; SEQ ID NO 202; 564pp; English.
XX
XX This invention relates to novel nucleic acid molecules isolated from
XX normal and neoplastic colon cells and the proteins encoded by them. The
XX invention may be useful for the production of compounds with a cytostatic
XX activity or for the development of a vaccine or gene therapy. The
XX invention may be useful for developing a treatment for a patient with
XX colon cancer, where the administration induces an immune response against
XX the colon cancer cell expressing the novel nucleic acids or proteins. The
XX invention may also be useful for diagnosing or monitoring the presence
XX and metastases of colon cancer in a patient. The present sequence is that
XX of a colon cancer cell-associated peptide of the invention.
XX

SQ Sequence 40 AA;

Query Match 100.0%; Score 23; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 62
AAU68589
ID AAU68589 standard; protein; 41 AA.
XX
AC AAU68589;
XX
XX 16-JAN-2002 (first entry)
XX
DE Human novel cytokine encoded by cDNA 790CIP2D_7 #2.
XX
XX Human; cytokine; cell proliferation; cell differentiation;
XX antiinflammatory; stem cell growth factor; activin; inhibin; cancer;
XX nervous system disease; neuropathy; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; spinal cord disorder;
XX head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
XX platelet disorder; thrombocytopaenia; stem cell disorder;
XX aplastic anaemia; tissue regeneration; wound healing; ulcer;
XX osteoporosis; osteoarthritis; bone degenerative disorder;
XX periodontal disease; fibrosis; reperfusion; immune disorder; SCID;
XX severe combined immunodeficiency; infection; autoimmune disorder;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
XX asthma; coagulation disorder; haemophilia; sepsis; nephritis;
XX inflammatory bowel disease; food supplement; immunogen.
XX
XX Homo sapiens.
XX
XX WO200175093-A1.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010484.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX 22-SEP-2000; 2000US-00668680.
XX
XX 23-OCT-2000; 2000US-00695618.
XX
XX 30-NOV-2000; 2000US-00728711.
XX
XX 14-MAR-2001; 2001US-00808701.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Aeundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX Xu C, Yang Y, Zhao QA, Chen R, Wang D, Goodrich RW, Liu C;
XX Drmanac RT;
XX
XX WPI: 2001-626432/72.
XX
XX N-PSDB; AAS59881.
XX
XX New polypeptides and nucleic acids, useful for diagnosis, treatment of
XX inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
XX degenerative disorders, cancer and promoting wound healing.
XX
XX Claim 20; Page 328; 336pp; English.
XX
XX The invention relates to isolated human polypeptides (which may be
XX cytokines) and the polynucleotides encoding them. The protein is useful
XX for identifying a compound which binds to it (e.g. modulators, agonists
XX and antagonists). The polynucleotides are useful as an array for mismatch
XX detection. The proteins and nucleic acids are useful as nutritional
XX sources or supplements. The protein exhibits activity relating
XX to cytokine, cell proliferation, cell differentiation, antiinflammatory,
XX stem cell growth factor activity, immune stimulating or immune

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suppressing and activin or inhibit related activities. The proteins (and antibodies raised against them) and nucleic acids are therefore useful in the diagnosis and treatment of diseases and disorders such as cancer, central and peripheral nervous system diseases and neuropathies, Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders, thrombocytopaenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence represents a novel protein of the invention

CC	The present invention relates to single exon nucleic acid probes (SEQ
CC	see AA131315-AA157546). The present sequence is a peptide encoded by
CC	this probe. The probes are useful for producing a microarray for
CC	predicting, measuring and displaying gene expression in samples derived
CC	from human placenta. The probes are useful for antenatal diagnosis of
CC	human genetic disorders
XX	
XX	
SQ	Sequence 41 AA;
	Query Match 100.0%; Score 23; DB 4; Length 41;
	Best Local Similarity 100.0%; Pred. No. 8.7e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 QGPR 4
Dd	12 GQPR 15
RESULT 64	
AAM91448	ID AAM91448 standard; protein; 41 AA.
XX	AAM91448;
XX	AC AC
XX	XX XX
DT	07-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen SEQ ID NO:19041.
XX	
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis.
XX	
OS	Homo sapiens.
XX	
PN	WO2001571182-A2.

PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231124P.
PR 08-SEP-2000; 2000US-02311243P.
PR 08-SEP-2000; 2000US-02311244P.
PR 08-SEP-2000; 2000US-0231141P.
PR 08-SEP-2000; 2000US-0231141P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-02311968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236700P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239353P.
PR 13-OCT-2000; 2000US-0239370P.
PR 20-OCT-2000; 2000US-0240360P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

N-PSDB; AAK64229.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11; SEQ ID NO 19041; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention

Sequence 41 AA;

Query Match 100.0%; Score 23; DB 4; Length 41;

Best Local Similarity 100.0%; Pred. No. 8.7e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 29 GQPR 32

RESULT 65

AAM64399

```

ID  AAM64399 standard; protein; 41 AA.
XX  AC
XX  AAM64399;
XX  DT
XX  05-NOV-2001 (first entry)
XX  DE
XX  Human brain expressed single exon probe encoded protein SEQ ID NO: 36504.
XX  Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO200157275-A2.
XX  PD
XX  09-AUG-2001.
XX  PF
XX  30-JAN-2001; 2001WO-US000667.
XX  PR
XX  04-FEB-2000; 2000US-0180312P.
XX  PR
XX  26-MAY-2000; 2000US-0207456P.
XX  PR
XX  30-JUN-2000; 2000US-00608408.
XX  PR
XX  03-AUG-2000; 2000US-00632366.
XX  PR
XX  21-SEP-2000; 2000US-0234687P.
XX  PR
XX  27-SEP-2000; 2000US-0236359P.
XX  PR
XX  04-OCT-2000; 2000GB-00024263.
XX  PA
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-483446/52.
XX  DR
XX  Single exon nucleic acid probes for analyzing gene expression in human
XX  brains.
XX  PT
XX  Example 4; SEQ ID NO 36504; 650pp + Sequence Listing; English.
XX  PS
XX  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  brain. They can be used to measure gene expression in brain cell samples,
XX  which may enable the diagnosis and improved treatment of nervous system
XX  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  epilepsy and cancers. The present sequence is a protein encoded by one of
XX  the probes of the invention
XX  SQ
XX  Sequence 41 AA;
XX  Query Match 100.0%; Score 23; DB 4; Length 41;
XX  Best Local Similarity 100.0%; Pred. No. 8.7e+02;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 1 GQPR 4
XX  DB 12 GQPR 15
XX  RESULT 66
XX  ABG58845
XX  ID ABG58845 standard; peptide; 41 AA.
XX  AC
XX  ABG58845;
XX  DT
XX  25-FEB-2003 (first entry)
XX  DE
XX  Human liver peptide, SEQ ID No 37493.
XX  KW
XX  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX  hypercholesterolaemia; coronary heart disease.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO200157273-A2.

XX  09-AUG-2001.
XX  PD
XX  AC
XX  AAM64399;
XX  DT
XX  05-NOV-2001 (first entry)
XX  DE
XX  Human brain expressed single exon probe encoded protein SEQ ID NO: 36504.
XX  Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO200157275-A2.
XX  PD
XX  09-AUG-2001.
XX  PF
XX  30-JAN-2001; 2001WO-US000664.
XX  PR
XX  04-FEB-2000; 2000US-0180312P.
XX  PR
XX  26-MAY-2000; 2000US-0207456P.
XX  PR
XX  30-JUN-2000; 2000US-00608408.
XX  PR
XX  03-AUG-2000; 2000US-00632366.
XX  PR
XX  21-SEP-2000; 2000US-0234687P.
XX  PR
XX  27-SEP-2000; 2000US-0236359P.
XX  PR
XX  04-OCT-2000; 2000GB-00024263.
XX  PA
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-488998/53.
XX  DR
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human adult liver.
XX  PS
XX  Claim 27; SEQ ID NO 37493; 658pp; English.
XX  CC
XX  The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX  measuring human gene expression in a sample derived from human adult
XX  liver, comprising one of 13109 defined nucleotide sequences given in the
XX  specification (or complements/ fragments). The probe hybridises at high
XX  stringency to a nucleic acid molecule expressed in the human adult liver.
XX  (I) may be used for predicting, measuring and displaying gene expression
XX  in samples derived from human adult liver. The genes identified may be
XX  involved in genetic liver diseases such as cirrhosis,
XX  hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX  associated with coronary heart disease. ABG47348-ABG59930 represent human
XX  liver single exon encoded peptides of the invention. Note: The sequence
XX  information for this patent does not appear in the printed specification
XX  but was obtained in electronic format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX  SQ
XX  Sequence 41 AA;
XX  Query Match 100.0%; Score 23; DB 4; Length 41;
XX  Best Local Similarity 100.0%; Pred. No. 8.7e+02;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 1 GQPR 4
XX  DB 12 GQPR 15
XX  RESULT 67
XX  ABG80821
XX  ID ABG80821 standard; protein; 42 AA.
XX  AC
XX  ABG80821;
XX  DT
XX  29-NOV-2002 (first entry)
XX  DE
XX  Rat SP-A mutant protein E195Q.
XX  KW
XX  Scaffold protein; C-type lectin-like domain; CTLD; alpha-helix;
XX  beta-strand; connecting segment; 14loop region; tetranectin;
XX  ligand-binding specificity; human; mouse; rat; chicken; mutant; mutuin.
XX  OS
XX  Rattus rattus.
XX  OS
XX  Synthetic.
XX  PN
XX  WO200248189-A2.
XX  XX
XX  20-JUN-2002.
XX  PF
XX  13-DEC-2001; 2001WO-DK000825.
XX  XX
```

PR 13-DEC-2000; 2000DK-00001872.
 PR 28-FEB-2001; 2001US-0272098P.
 XX (BORE-) BOREAN PHARMA AS.
 PA Etzerodt M, Holtet TL, Gravarsen NJH, Thogersen HC;
 XX WPI; 2002-6432278/69.
 XX WPI; 2002-6432278/69.
 XX Protein comprising a variant of model C-type lectin-like domains (CTLTD),
 PT in which alpha helices, beta-strands, connecting segments are conserved,
 PT to maintain CTLTD scaffold structure, while the loop region is altered.
 XX
 PS Claim 1; Page 17; 168pp; English.
 XX The present invention relates to a new protein with scaffold structure of
 CC C-type lectin-like domains (CTLTD). The invention comprises a variant of a
 CC model CTLTD where alpha-helices and beta-strands and connecting segments
 CC are conserved such that scaffold structure of C-type lectin-like domains
 CC (CTLTD) is substantially maintained, while the 14loop region is altered by
 CC amino acid substitution, deletion, insertion or their combination. The
 CC invention is useful for preparing a library of nucleotide sequences
 CC encoding related proteins by randomising part or all of the nucleic acid
 CC sequence encoding the loop region of its CTLTD. The artificial CTLTD
 CC protein products are preferable to antibody derivatives as each binding
 CC site is a single structurally autonomous protein domain. When used as
 CC components of compositions to be used for in vivo diagnostic or
 CC therapeutic purposes, artificial CTLTD protein products constructed on the
 CC basis of human CTLTDs are virtually identical to the corresponding natural
 CC CTLTD protein already present in the body and are therefore less
 CC immunogenic to the patient. They also have a smaller size, and thus
 CC provide tissue penetration and distribution, as well as shorter half life
 CC in circulation. Since murine and human tetranectin are identical in
 CC structure, straightforward swapping of polypeptide segments defining
 CC ligand-binding specificity between murine and human tetranectin
 CC derivatives may be achieved. The present amino acid sequence represents a
 CC mutant protein of the invention
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 23; DB 5; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 29 GQPR 32
 RESULT 68
 AD97549
 ID ADS97549 standard; protein; 42 AA.
 XX ADS97549;
 AC
 XX 16-DEC-2004 (first entry)
 DT
 XX Dementia related secretogranin 1 peptide DRES-15.
 DE
 XX DRES-15; dementia related secretogranin 1; secretogranin 1;
 KW Alzheimer's disease; diagnosis; gene therapy; human; marker.
 KW Homo sapiens.
 XX WO2004082455-A2.
 PN 30-SEP-2004.
 XX 18-MAR-2004; 2004WO-EP002824.
 XX 18-MAR-2003; 2003EP-00005968.
 PR 07-JAN-2004; 2004EP-00000170.
 XX

(BIOV-) BIOVISION AG.
 PA Lamping N, Zucht H, Selle H, Juergens M, Heine G, Hess R;
 XX Kellmann M, Lamerz J, Moehring T;
 PI WPI; 2004-718701/70.
 XX Detecting a neurological disease, particularly Alzheimer's disease,
 PT comprises determining at least one dementia related secretogranin 1
 PT (DRES) peptide, or at least one peptide corresponding to GeneBank
 PT Accession No NM001819.
 XX Claim 1; SEQ ID NO 15; 110pp; English.
 PS The present sequence is that of dementia related secretogranin 1 peptide
 CC DRES-15 (mass 4583.1 Da), corresponding to amino acids 217-258 of human
 CC secretogranin 1 ADS97579 and optionally including a phosphorylated or
 CC sulfated residue. The peptide can be used as a marker in claimed methods
 CC of the invention for detecting a neurological disease, preferably
 CC Alzheimer's disease (AD), or a predisposition to such a disease.
 CC Detection of AD is based on the finding that the concentration of certain
 CC peptides is changed in bodily fluid samples, especially in the
 CC cerebrospinal fluid, of AD patients relative to their concentration in
 CC control samples. A method for detecting a neurological disease, in
 CC particular a chronic dementia disease, especially AD or a predisposition
 CC to such a disease involves the detection of at least one DRES peptide
 CC ADS97535-ADS97578 and ADS97581-ADS97591 in a biological sample.
 CC Preferably, the peptide(s) is determined in combination with one or more
 CC peptides derived from chromogranin A ADS97606-ADS97619, secretogranin 2
 CC ADS97595-ADS97605 and/or secretogranin 5 ADS97592-ADS97594. The disease
 CC can be detected at an early stage e.g. in the diagnosis of mild cognitive
 CC impairment, or in neurological diseases other than AD, such as Lewy body
 CC dementia, vascular dementia or depression. Determination of the marker
 CC peptides is conducted by an activity, immunological, molecular
 CC biological, physical or chemical assay. Preferably the mass of the
 CC peptide is determined by mass spectrometry. Pharmaceutical products
 CC comprise the marker peptides, antibodies directed to the peptides,
 CC nucleic acids corresponding to the peptides, a ribozyme, antisense
 CC nucleic acid, triplex-forming nucleic acid or RNAi nucleic acid, peptide
 CC antagonists or peptide agonists for the therapy, diagnosis, prognosis or
 CC prophylaxis of neurological diseases, particularly AD. The marker
 CC peptides may be mutated at 1 or 2 amino acid positions corresponding to
 CC the non-mutated DRES sequence, or chemically or enzymatically modified,
 CC or post-translationally modified, preferably phosphorylated, sulfated,
 CC oxidised or C-terminally amidated, or have a pyroglutamate modification
 CC in an individual's biological sample.
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 23; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 39 GQPR 42
 RESULT 69
 AAR95499
 ID AAR95499 standard; peptide; 43 AA.
 XX AAR95499;
 AC
 XX 06-NOV-1996 (first entry)
 DT
 XX E85, monoclonal antibody SM-3 derived antigen binding peptide.
 DE
 XX Abtide; prostate specific mucin antigen; human prostate cancer; LNCaP;
 KW diagnostic; detection; imaging; tumour; phage; peptide library; breast;
 KW polymorphic; epithelial.
 XX
 OS Synthetic.

```

XX PN W09609411-A1.
XX PD 28-MAR-1996.
XX PF 20-SEP-1995; 95WO-US011934.
XX PR 21-SEP-1994; 94US-00310192.
XX PR 07-JUN-1995; 95US-00488161.
XX PA (CYTO-) CYTOGEN CORP.
XX PI Alvarez VL;
XX WPI; 1996-188471/19.
XX PT New isolated peptide(s) with specific binding activities - obtcd. by
XX screening random peptide libraries, for use in diagnostic and therapeutic
XX compens.
XX Claim 39; Page 78; 106pp; English.
XX AAR95459-R95509 are antigen binding peptides ("abtides") derived from the
XX monoclonal antibody SM-3 which recognises a specific polymorphic
XX epithelial mucin tumour antigen found on human breast cancer cells. The
XX abtides are identified from random peptide libraries using specific
XX ligand binding. Abtides mimic the binding specificity of large molecules
XX such as antibodies and receptors but have a much smaller size allowing
XX their production at a lower cost and reducing the extent of their
XX immunogenicity aiding in vivo delivery. The abtides are useful for the
XX diagnosis, detection, imaging and treatment of disease, e.g. tumours,
XX prostate cancer and breast cancer
XX SQ Sequence 43 AA;
XX Query Match 100.0%; Score 23; DB 2; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 9.1e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GQPR 4
XX Db |||||
XX 7 GQPR 10
XX
XX RESULT 71
XX AAE21238
XX ID AAE21238 standard; peptide; 43 AA.
XX AC AAE21238;
XX DT 01-JUL-2002 (first entry)
XX DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:103.
XX KW Human; secreted protein; gene therapy; human immunodeficiency virus; HIV;
XX immune disease; autoimmune disease; anaemia; multiple sclerosis; cancer;
XX rheumatoid arthritis; hyperproliferative disorder; melanoma; neoplasm;
XX seazay syndrome; Gaucher's disease; neurological disease; cardiac arrest;
XX Alzheimer's disease; Parkinson's disease; Charcot-Marie-Tooth disease;
XX cardiovascular disorder; cerebrovascular disorder; tachycardia; angina;
XX thrombosis; ocular disorder; corneal infection; wound healing; cardiant;
XX vascular; thrombolytic; cytostatic; nootropic.
XX OS Homo sapiens.
XX PN W0200216390-A1.
XX PD 28-FEB-2002.
XX PF 17-JAN-2001; 2001WO-US001435.
XX PR 18-AUG-2000; 2000US-0226282P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX QY 1 GQPR 4
XX Db |||||
XX 7 GQPR 10
XX
XX RESULT 71
XX AAE21238
XX ID AAE21238 standard; protein; 43 AA.
XX AC AAE21238;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #26412.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN W0200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.

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DR N-PSDB; AAS90608.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 20; SEQ ID NO 56780; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 43 AA;

XX Query Match 100.0%; Score 23; DB 4; Length 43;

XX Best Local Similarity 100.0%; Pred. No. 9.1e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 GQPR 4

XX Db |||||

XX 7 GQPR 10

XX

XX RESULT 71

XX AAE21238

XX ID AAE21238 standard; peptide; 43 AA.

XX AC AAE21238;

XX DT 01-JUL-2002 (first entry)

XX DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:103.

XX KW Human; secreted protein; gene therapy; human immunodeficiency virus; HIV;

XX immune disease; autoimmune disease; anaemia; multiple sclerosis; cancer;

XX rheumatoid arthritis; hyperproliferative disorder; melanoma; neoplasm;

XX seazay syndrome; Gaucher's disease; neurological disease; cardiac arrest;

XX Alzheimer's disease; Parkinson's disease; Charcot-Marie-Tooth disease;

XX cardiovascular disorder; cerebrovascular disorder; tachycardia; angina;

XX thrombosis; ocular disorder; corneal infection; wound healing; cardiant;

XX vascular; thrombolytic; cytostatic; nootropic.

XX OS Homo sapiens.

XX PN W0200216390-A1.

XX PD 28-FEB-2002.

XX PF 17-JAN-2001; 2001WO-US001435.

XX PR 18-AUG-2000; 2000US-0226282P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX QY 1 GQPR 4

XX Db |||||

XX 7 GQPR 10

XX

XX RESULT 71

XX AAE21238

XX ID AAE21238 standard; protein; 43 AA.

XX AC AAE21238;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #26412.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN W0200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J;
XX WPI; 2002-304113/34.
XX An isolated nucleic acid molecule (I) comprising a polynucleotide which
PT encodes a polypeptide useful in the diagnosis and treatment of disorders
PT e.g. immune disorders.
XX
XX Disclosure; Page 7; 504pp; English.
XX
XX AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
CC protein genes, and AAE21191-AAE21235 represent the proteins they encode.
CC AAE21236-AAE21280 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 21 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of immune
CC or autoimmune diseases e.g. AIDS (acquired immune deficiency syndrome),
CC asthma, anaemia and rheumatoid arthritis, breast neoplasia and breast
CC cancer, neurological diseases e.g. Alzheimer's disease, Parkinson's
CC disease, Huntington's disease, Tourette syndrome, meningitis,
CC demyelinating disease, peripheral neuropathies, neoplasia, trauma,
CC congenital malformations, spinal cord injuries, toxic neuropathies
CC induced by neurotoxins, peripheral neuropathies, multiple sclerosis,
CC ischaemia and infarction, haemorrhages, schizophrenia, mania, dementia,
CC depression, panic disorder, learning disabilities, ALS, altered
CC behaviours e.g. disorders in feeding, sleep patterns, balance and
CC perception, encephalitis, disorders in cardiovascular, neural/sensory,
CC reproductive and digestive systems, behavioural disorders and
CC hyperproliferative disorder. The present sequence represents human
CC secreted protein fragment referred to in the disclosure of the invention
XX
XX Sequence 43 AA;
SQ
Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db ||||
10 GQPR 13
RESULT 72
ADI21604
ID ADI21604 standard; protein; 43 AA.
XX
XX ADI21604;
XX
XX 15-APR-2004 (first entry)
XX
XX Novel human polypeptide #83.
DE
XX forensic; nutritional source; damaged tissue; diseased tissue;
XX myeloid cell disorder; lymphoid cell disorder;
XX bone cartilage tissue growth; tendon tissue growth;
XX ligament tissue growth; nerve tissue growth; regeneration; wound healing;
XX tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
XX
XX Homo sapiens.
OS
XX WO2003025148-A2.
XX
XX 27-MAR-2003.
XX
XX 19-SEP-2002; 2002WO-US029964.
XX
XX 19-SEP-2001; 2001US-0323739P.
XX
XX 19-SEP-2002; 2002US-00323739P.
PR

PR 13-SEP-2002; 2002US-00323739.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX
XX WPI; 2003-354603/33.
DR N-PSDB; ADI21384.
XX
XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.
XX
XX Example 3; SEQ ID NO 855; 156pp; English.
PS
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents the amino acid sequence of a novel human
CC polypeptide.
XX
XX Sequence 43 AA;
SQ
Query Match 100.0%; Score 23; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db ||||
7 GQPR 10
RESULT 73
ADI21603
ID ADI21603 standard; protein; 43 AA.
XX
XX ADI21603;
XX
XX 15-APR-2004 (first entry)
XX
XX Novel human polypeptide #82.
DE
XX forensic; nutritional source; damaged tissue; diseased tissue;
XX myeloid cell disorder; lymphoid cell disorder;
XX bone cartilage tissue growth; tendon tissue growth;
XX ligament tissue growth; nerve tissue growth; regeneration; wound healing;
XX tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
XX
XX Homo sapiens.
OS
XX WO2003025148-A2.
XX
XX 27-MAR-2003.
XX
XX 19-SEP-2002; 2002WO-US029964.
XX
XX 19-SEP-2001; 2001US-0323739P.
XX
XX 13-SEP-2002; 2002US-00323739.
PR


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PA (HYSE-) HYSEQ INC.
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX WPI; 2003-354603/33.
DR N-PSDB; ADI21383.
DR
XX
XX
XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.
XX
XX Example 3; SEQ ID NO 854; 156pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents the amino acid sequence of a novel human
CC polypeptide.
XX
XX Sequence 43 AA;
SQ

```

Query Match 100.0%; Score 23; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GQPR 4
DB 7 GQPR 10

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RESULT 74
AM89537
ID AM89537 standard; protein; 44 AA.
XX
AC AM89537;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:17130.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
XX Homo sapiens.
OS
XX WO200157182-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
PF 17-JAN-2001; 2001WO-US0001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184564P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.

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07-JUN-2000; 2000US-0209467P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225213P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225267P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225759P.
18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226688P.
22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-0229287P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0232080P.
08-SEP-2000; 2000US-0232081P.
12-SEP-2000; 2000US-0231968P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233064P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX N-PSDB; AAK62318.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX Claim 11; SEQ ID NO 17130; 3071pp + Sequence Listing; English.
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For

CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 44 AA;
 Query Match 100.0%; Score 23; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 25 GQPR 28
 RESULT 75
 ID AAO03183 standard; protein; 44 AA.
 XX AAO03183;
 XX 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 17075.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX Homo sapiens.
 XX WO200164835-A2.
 PD 07-SEP-2001.
 XX 26-FEB-2001; 2001WO-US004927.
 XX 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AAI83114.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX Claim 20; SEQ ID NO 17075; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 44 AA;
 Query Match 100.0%; Score 23; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 ||||
 Db 2 GQPR 5

Search completed: May 17, 2005, 10:07:08
 Job time : 222 secs

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OM protein - protein search, using sw model

Run on: May 17, 2005, 09:59:07 ; Search time 16 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-10-731-921-3
Perfect score: 23
Sequence: 1 GQPR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	27	F70540	hypothetical prote
2	23	100.0	63	F98129	hypothetical prote
3	23	100.0	65	AE2406	hypothetical prote
4	23	100.0	67	F84040	hypothetical prote
5	23	100.0	89	T51191	small zinc finger-
6	23	100.0	89	T51192	small zinc finger-
7	23	100.0	90	AD0847	hydrogenase isoenz
8	23	100.0	90	S15199	hydrogenase expres
9	23	100.0	90	H85921	pleiotrophic effec
10	23	100.0	90	H91076	hydrogenase isoenz
11	23	100.0	91	AG2217	hypothetical prote
12	23	100.0	98	D72601	hypothetical prote
13	23	100.0	101	G97567	hypothetical prote
14	23	100.0	101	AF2788	hypothetical prote
15	23	100.0	101	F75500	hypothetical prote
16	23	100.0	102	S19733	hypothetical prote
17	23	100.0	102	I39621	rbpA1 protein - An
18	23	100.0	102	ASL899	RNA-binding protei
19	23	100.0	104	1 ASLJSY	vpr protein - huma
20	23	100.0	106	G84541	hypothetical prote
21	23	100.0	109	H72687	hypothetical prote
22	23	100.0	109	C83432	conserved hypotet
23	23	100.0	115	T46397	hypothetical prote
24	23	100.0	115	AG0688	probable bacteriop
25	23	100.0	118	S14079	pim1 protein - mou
26	23	100.0	122	E75464	hypothetical prote
27	23	100.0	126	H95343	hypothetical prote
28	23	100.0	128	A98346	hypothetical prote
29	23	100.0	129	H81809	hypothetical prote

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33	23	100.0	135	H84961	hypothetical prote
34	23	100.0	138	C72713	hypothetical prote
35	23	100.0	138	AB0699	probable pathogeni
36	23	100.0	139	T48793	hypothetical prote
37	23	100.0	139	T25747	hypothetical prote
38	23	100.0	139	AH3415	hypothetical membr
39	23	100.0	140	I46880	T-cell receptor be
40	23	100.0	140	E83391	probable ring-clea
41	23	100.0	141	H75383	hypothetical prote
42	23	100.0	144	E84219	hypothetical prote
43	23	100.0	145	F83267	conserved hypotet
44	23	100.0	147	S76050	hypothetical prote
45	23	100.0	148	E86741	hypothetical prote
46	23	100.0	149	S74366	hypothetical prote
47	23	100.0	150	AE2595	hypothetical prote
48	23	100.0	151	D70677	hypothetical prote
49	23	100.0	152	F72764	hypothetical prote
50	23	100.0	153	C83004	probable rRNA meth
51	23	100.0	157	AE3240	conserved hypotet
52	23	100.0	157	E75530	hypothetical prote
53	23	100.0	161	AF2936	hypothetical prote
54	23	100.0	162	E69155	hypothetical prote
55	23	100.0	165	T46052	ADP-ribosylation f
56	23	100.0	166	B97639	hypothetical prote
57	23	100.0	166	AC2862	ureidoglycolate hy
58	23	100.0	166	H86243	hypothetical prote
59	23	100.0	168	E75257	molybdenum cofacto
60	23	100.0	170	G95987	probable ureidogly
61	23	100.0	171	B87593	hypothetical prote
62	23	100.0	171	T50632	hypothetical prote
63	23	100.0	176	B75494	conserved hypotet
64	23	100.0	176	F83819	hypothetical prote
65	23	100.0	177	T08126	pathogenesis-relat
66	23	100.0	177	T19610	hypothetical prote
67	23	100.0	184	H87430	flagellin modifca
68	23	100.0	185	T27225	ADP-ribosylation f
69	23	100.0	185	T34807	probable transcrip
70	23	100.0	186	B82649	hypothetical prote
71	23	100.0	190	T46053	ADP-ribosylation f
72	23	100.0	191	A75518	guanyl-specific ri
73	23	100.0	196	A83008	conserved hypotet
74	23	100.0	197	H87446	potassium-transpor
75	23	100.0	200	B96902	probable NADPH-qui
76	23	100.0	201	F97063	surfactin biosynth
77	23	100.0	201	A83599	hypothetical prote
78	23	100.0	204	B72350	hypothetical prote
79	23	100.0	205	F82562	hypothetical prote
80	23	100.0	205	B82562	hypothetical prote
81	23	100.0	207	A98123	hypothetical prote
82	23	100.0	207	H85967	hypothetical prote
83	23	100.0	207	D65095	hypothetical prote
84	23	100.0	207	T49218	hypothetical prote
85	23	100.0	208	1 VCVQL2	coat protein - pot
86	23	100.0	208	1 VCVQWA	coat protein - pot
87	23	100.0	208	F75427	mazG protein - Del
88	23	100.0	208	S24593	hypothetical prote
89	23	100.0	208	S41878	coat protein - pot
90	23	100.0	208	S41874	coat protein - pot
91	23	100.0	208	T46927	hypothetical prote
92	23	100.0	209	T48225	hypothetical prote
93	23	100.0	212	T18943	hypothetical prote
94	23	100.0	212	T46271	hypothetical prote
95	23	100.0	213	A75471	probable nitrogen
96	23	100.0	213	C70943	hypothetical prote
97	23	100.0	213	T47135	hypothetical prote
98	23	100.0	216	D72587	phosphoesterase-re
99	23	100.0	217	T47175	hypothetical prote
100	23	100.0	217	A98196	hypothetical prote
101	23	100.0	218	A36040	Ig heavy chain V-I
102	23	100.0	218	F72169	A49L protein - var

103	23	100.0	218	2	T28586	16L protein - vari	176	23	100.0	277	2	S40167	hypothetical prote
104	23	100.0	218	2	B36853	A46L protein - var	177	23	100.0	277	2	A49890	fdxh 5'-region hyp
105	23	100.0	219	2	H72615	hypothetical prote	178	23	100.0	277	2	A32642	protein yb18 precu
106	23	100.0	219	2	T37426	probable 25.1k pro	179	23	100.0	278	2	F82299	dihydropteroate sy
107	23	100.0	219	2	G42521	A41L protein - vac	180	23	100.0	278	2	E87704	hypothetical prote
108	23	100.0	219	2	JQ1778	SalF3L protein pre	181	23	100.0	278	2	S30124	hypothetical prote
109	23	100.0	219	2	G89791	conserved hypothet	182	23	100.0	279	2	T37010	probable DNA-bindi
110	23	100.0	220	2	S25245	rep protein - Bord	183	23	100.0	279	2	AD2663	transcription regu
111	23	100.0	221	2	PQ0764	chlorophyll a/b-bi	184	23	100.0	282	2	T34934	hypothetical prote
112	23	100.0	221	2	AG1961	hypothetical prote	185	23	100.0	283	2	F97357	stage 0 sporulatio
113	23	100.0	223	2	T19194	hypothetical prote	186	23	100.0	283	2	A98340	hypothetical prote
114	23	100.0	224	2	T19190	hypothetical prote	187	23	100.0	285	2	S08491	hypothetical prote
115	23	100.0	224	2	AH0875	probable membrane	188	23	100.0	287	2	T27056	hypothetical prote
116	23	100.0	225	2	A86043	probable transposa	189	23	100.0	289	1	G3HUI	Ig gamma-3 heavy c
117	23	100.0	226	2	T43115	IS946 transposase	190	23	100.0	289	2	T36187	hypothetical prote
118	23	100.0	226	2	A43948	transposase - Lact	191	23	100.0	290	2	E83331	transcription regu
119	23	100.0	226	2	A34023	probable transposa	192	23	100.0	291	2	S15927	sflah protein precu
120	23	100.0	226	2	A37751	probable transposa	193	23	100.0	293	2	G82997	probable transcrip
121	23	100.0	226	2	S25777	hypothetical prote	194	23	100.0	296	1	MMADL2	late 100K protein
122	23	100.0	227	1	H84387	probable phosphos	195	23	100.0	297	2	T18660	hypothetical prote
123	23	100.0	227	1	S68150	eosinophil major b	196	23	100.0	297	2	B70685	hypothetical prote
124	23	100.0	228	2	T11130	cytochrome-c oxida	197	23	100.0	298	2	AG3531	high-affinity zinc
125	23	100.0	230	2	B95337	hypothetical prote	198	23	100.0	298	2	C97445	transcription regu
126	23	100.0	232	2	I46679	alpha-smooth muscl	199	23	100.0	299	2	C49233	S fimbrial adhesin
127	23	100.0	232	2	H75274	polypeptide deform	200	23	100.0	299	2	I76900	F1652 minor fimbri
128	23	100.0	232	2	T43098	transposase - Lact	201	23	100.0	300	2	G70719	hypothetical prote
129	23	100.0	233	1	A73174	probable phosphos	202	23	100.0	303	2	A71557	probable pseudouri
130	23	100.0	233	1	H71040	probable phosphos	203	23	100.0	304	2	H96528	hypothetical prote
131	23	100.0	234	2	PT0207	Ig gamma chain C r	204	23	100.0	305	2	T31740	hypothetical prote
132	23	100.0	237	2	B84377	hypothetical prote	205	23	100.0	307	2	H75405	probable singlet o
133	23	100.0	238	2	T27044	hypothetical prote	206	23	100.0	308	2	H70852	probable lipR prot
134	23	100.0	238	2	G83031	probable ATP-bindi	207	23	100.0	308	2	AE2359	hypothetical prote
135	23	100.0	238	2	AG3111	hypothetical prote	208	23	100.0	309	2	T47685	probable RNA bindi
136	23	100.0	243	1	H64413	probable phosphos	209	23	100.0	310	2	AC1859	hypothetical prote
137	23	100.0	243	1	H82767	hypothetical prote	210	23	100.0	310	2	T26710	hypothetical prote
138	23	100.0	244	2	AG1013	probable exported	211	23	100.0	311	2	T15997	hypothetical prote
139	23	100.0	244	2	T33066	hypothetical prote	212	23	100.0	312	1	S74432	hypothetical prote
140	23	100.0	245	1	C65210	hypothetical 26.3	213	23	100.0	312	2	A61183	hypothetical prote
141	23	100.0	245	2	S19018	complement subcomp	214	23	100.0	313	2	G69064	hypothetical prote
142	23	100.0	245	2	S06329	chlorophyll a/b-bi	215	23	100.0	313	2	D69945	phage-related prot
143	23	100.0	245	2	S28827	chlorophyll a/b-bi	216	23	100.0	314	2	AB2409	dTDP-glucose dehyd
144	23	100.0	245	2	C91255	hypothetical prote	217	23	100.0	314	2	C70692	hypothetical prote
145	23	100.0	245	2	G86095	hypothetical prote	218	23	100.0	315	2	T47181	hypothetical prote
146	23	100.0	246	2	S00443	hypothetical prote	219	23	100.0	315	2	F98295	hypothetical prote
147	23	100.0	246	2	S17694	chlorophyll a/b-bi	220	23	100.0	316	2	S29394	l-arginase - Afric
148	23	100.0	248	2	B95334	probable transcrip	221	23	100.0	317	2	H70566	hypothetical prote
149	23	100.0	249	2	S69340	Ig heavy chain VHI	222	23	100.0	317	1	RMRBB	T-cell receptor be
150	23	100.0	250	2	JQ1881	hypothetical 27.1k	223	23	100.0	319	2	H87035	RNA polymerase sig
151	23	100.0	253	1	E75287	probable phosphos	224	23	100.0	319	2	S61293	transcription init
152	23	100.0	254	2	G76814	hypothetical prote	225	23	100.0	320	2	T30894	lipase homolog TO
153	23	100.0	255	2	G75626	probable 3-alpha-h	226	23	100.0	322	1	A26370	arginase (EC 3.5.3
154	23	100.0	255	2	F98175	hypothetical prote	227	23	100.0	323	1	A26702	arginase (EC 3.5.3
155	23	100.0	255	4	S31866	Ig gamma-1 chain C	228	23	100.0	323	2	JC5011	transcription init
156	23	100.0	256	2	E95912	probable acetyltra	229	23	100.0	325	2	E75404	ABC transporter, A
157	23	100.0	256	2	A35340	H+-transporting tw	230	23	100.0	325	2	S75747	hypothetical prote
158	23	100.0	258	2	D95421	conserved hypothet	231	23	100.0	325	2	T18594	hypothetical prote
159	23	100.0	260	2	E83174	hypothetical prote	232	23	100.0	326	1	G2HU	Ig gamma-2 chain C
160	23	100.0	261	2	T04301	beta-expansin - ri	233	23	100.0	326	2	A96608	hypothetical prote
161	23	100.0	261	2	T75926	hypothetical prote	234	23	100.0	327	1	G4HU	Ig gamma-4 chain C
162	23	100.0	263	2	C95942	probable transcrip	235	23	100.0	327	2	T27042	hypothetical prote
163	23	100.0	263	4	I67792	probable glucosylc	236	23	100.0	330	1	GHU	Ig gamma-1 chain C
164	23	100.0	264	2	S04046	embryonic abundant	237	23	100.0	332	2	G65187	hypothetical prote
165	23	100.0	265	2	T33012	hypothetical prote	238	23	100.0	333	2	A95844	probable transcrip
166	23	100.0	265	2	A12942	conserved hypothet	239	23	100.0	334	2	S35015	regulatory protein
167	23	100.0	266	2	S60674	hypothetical prote	240	23	100.0	334	2	S74737	conserved hypothet
168	23	100.0	266	2	H83517	probable transcrip	241	23	100.0	335	2	B82220	hypothetical prote
169	23	100.0	269	2	AB2124	hypothetical prote	242	23	100.0	336	2	F89530	protein H28G03.1 f
170	23	100.0	269	2	S73616	MG374 homolog G12	243	23	100.0	338	2	B98195	hypothetical prote
171	23	100.0	271	2	P84442	hypothetical prote	244	23	100.0	338	2	AH3091	conserved hypothet
172	23	100.0	272	2	AC2037	hypothetical prote	245	23	100.0	338	2	G82643	conserved hypothet
173	23	100.0	272	2	AB2988	conserved hypothet	246	23	100.0	339	2	A30754	hypothetical prote
174	23	100.0	273	2	JQ0418	pyrrolidine-5-carbox	247	23	100.0	341	2	H90797	probable tellurium
175	23	100.0	275	1	E64117	dihydropteroate sy	248	23	100.0	341	2	A83644	hypothetical prote

249	23	100.0	342	2	S23438	hypothetical prote	342	23	100.0	429	2	B83257	folypolyglutamate
250	23	100.0	342	2	S53663	hydrogenase-relate	323	23	100.0	433	2	B81992	NADH2 dehydrogenas
251	23	100.0	344	2	G70726	DNA-binding protei	324	23	100.0	433	2	B81222	NADH dehydrogenase
252	23	100.0	346	2	G69325	LPS glycosyltransf	325	23	100.0	434	2	AC2733	NADH ubiquinone ox
253	23	100.0	346	2	E83759	cytochrome d (bd-c	326	23	100.0	434	2	E97514	NADH dehydrogenase
254	23	100.0	349	2	C86969	Holliday junction	327	23	100.0	435	2	AC3396	NADH2 dehydrogenas
255	23	100.0	350	2	H81272	3-isopropylmalate	328	23	100.0	436	2	B70510	probable acyltrans
256	23	100.0	351	2	H81028	fatty acid/phospho	329	23	100.0	439	2	F87490	NADH dehydrogenase
257	23	100.0	351	2	F81972	probable fatty aci	330	23	100.0	441	2	E87214	hypothetical prote
258	23	100.0	354	2	B72363	3-isopropylmalate	331	23	100.0	443	2	S72905	phosphate sensor p
259	23	100.0	355	2	G95332	probable adenylate	332	23	100.0	444	2	H82821	NADH-ubiquinone ox
260	23	100.0	357	2	E82564	3-isopropylmalate	333	23	100.0	444	2	F75387	NADH dehydrogenase
261	23	100.0	358	1	JX0286	3-isopropylmalate	334	23	100.0	444	2	S64912	probable membrane
262	23	100.0	358	2	JQ2348	hypothetical 41.2K	335	23	100.0	445	1	G70647	NADH2 dehydrogenas
263	23	100.0	360	2	D83255	phosphate carrier	336	23	100.0	445	2	S76019	ATP-dependent clp
264	23	100.0	361	2	B53737	mannose-1-phosphat	337	23	100.0	445	2	JQ2264	canavalin - jack b
265	23	100.0	361	2	T01007	phosphoserine amin	338	23	100.0	445	2	S00281	canavalin - sword
266	23	100.0	362	2	C82572	phosphate carrier	339	23	100.0	445	2	E70854	probable membrane
267	23	100.0	362	2	A53737	triacylglycerol li	340	23	100.0	449	2	T34619	NADH2 dehydrogenas
268	23	100.0	363	2	A34959	mannose-1-phosphat	341	23	100.0	451	2	A70539	hypothetical prote
269	23	100.0	364	2	T47698	hypothetical sugar	342	23	100.0	453	2	AE0774	probable protease
270	23	100.0	366	2	E95856	hypothetical prote	343	23	100.0	453	2	H64974	hypothetical prote
271	23	100.0	367	2	G83368	DNA-binding protei	344	23	100.0	453	2	A98990	hypothetical prote
272	23	100.0	369	2	F27734	teichoic acid bios	345	23	100.0	453	2	D85835	hypothetical prote
273	23	100.0	369	2	F69146	conserved hypotet	346	23	100.0	454	2	AH2754	two component resp
274	23	100.0	370	2	F87638	hypothetical prote	347	23	100.0	454	2	F97535	nitrogen assimilat
275	23	100.0	371	2	S23861	hypothetical prote	348	23	100.0	454	2	E70637	hypothetical prote
276	23	100.0	374	2	S69339	Ig heavy chain v r	349	23	100.0	454	2	E70503	hypothetical prote
277	23	100.0	374	2	B54800	thin filament-asso	350	23	100.0	456	2	H86406	probable serine ca
278	23	100.0	375	2	T28710	hypothetical prote	351	23	100.0	458	2	F84746	collagenase prtC h
279	23	100.0	375	2	F75467	probable lipoprote	352	23	100.0	460	2	G24066	hypothetical prote
280	23	100.0	375	2	A46174	RNA-binding protei	353	23	100.0	460	2	T23667	sensor protein Cpx
281	23	100.0	376	1	ATR23	actin 3 - rice	354	23	100.0	464	2	C82046	probable peptidase
282	23	100.0	376	2	G70800	probable ABC trans	355	23	100.0	464	2	C82967	probable proteinas
283	23	100.0	377	2	A23511	Ig gamma-3 chain C	356	23	100.0	464	2	AG0347	hypothetical prote
284	23	100.0	377	2	A60764	Ig gamma-3 chain C	357	23	100.0	464	2	T50955	transcription init
285	23	100.0	377	2	E69688	response regulator	358	23	100.0	466	1	S61292	beta-fructofuranos
286	23	100.0	382	2	D75398	hypothetical prote	359	23	100.0	466	2	S62330	probable proteinas
287	23	100.0	384	2	T39377	conserved hypotet	360	23	100.0	466	2	F82288	conserved hypotet
288	23	100.0	384	2	AH1826	hypothetical prote	361	23	100.0	467	2	A82664	triglycer factor lim
289	23	100.0	385	2	A85607	hypothetical prote	362	23	100.0	471	2	AB2266	hypothetical prote
290	23	100.0	386	2	T49275	serine C-palmitoyl	363	23	100.0	475	2	T27725	protein-tyrosine k
291	23	100.0	387	2	A82649	hypothetical prote	364	23	100.0	477	1	TVMVCS	probable lyase PA3
292	23	100.0	391	2	T31251	aromatic oxygenase	365	23	100.0	477	2	G83205	cationic amino aci
293	23	100.0	392	2	AG0226	probable exported	366	23	100.0	477	2	D82587	interferon-induced
294	23	100.0	392	2	S72436	RNA-binding protei	367	23	100.0	478	2	A25407	hypothetical prote
295	23	100.0	393	2	I53063	testicular tumor p	368	23	100.0	481	2	T32260	hypothetical prote
296	23	100.0	394	2	AB2747	lipid A-disacchari	369	23	100.0	481	2	S76115	hypothetical prote
297	23	100.0	394	2	A97528	lipid a-disacchari	370	23	100.0	482	2	E70554	hypothetical prote
298	23	100.0	395	2	T36852	probable integral	371	23	100.0	484	2	S23817	hypothetical prote
299	23	100.0	395	2	C71148	hypothetical prote	372	23	100.0	485	2	S75655	anthranilate synth
300	23	100.0	398	2	S16275	naringenin-chalcon	373	23	100.0	488	2	D70876	probable polyketid
301	23	100.0	398	2	S58190	naringenin-chalcon	374	23	100.0	488	2	I56507	histamine Hi recep
302	23	100.0	399	2	F69034	argininosuccinate	375	23	100.0	489	2	T49274	serine C-palmitoyl
303	23	100.0	402	2	T21278	hypothetical prote	376	23	100.0	489	2	T46450	hypothetical prote
304	23	100.0	403	2	G71564	hypothetical prote	377	23	100.0	497	1	G02938	probable debrisocu
305	23	100.0	406	2	T29521	hypothetical prote	378	23	100.0	497	1	O4HUD1	debrisoquine 4-hyd
306	23	100.0	408	2	D70549	hypothetical prote	379	23	100.0	497	2	F86712	di-/tripeptide tra
307	23	100.0	408	2	H87193	probable FAD-linke	380	23	100.0	500	1	D31579	cytochrome P450 2D
308	23	100.0	409	2	B69147	teichoic acid bios	381	23	100.0	500	1	JC4153	cytochrome P450 2D
309	23	100.0	410	2	E72397	hypothetical prote	382	23	100.0	500	1	JC4157	cytochrome P450 2D
310	23	100.0	411	2	I38873	serine C-palmitoyl	383	23	100.0	500	1	JE0258	cytochrome P450 2D
311	23	100.0	412	2	S76239	hypothetical prote	384	23	100.0	500	1	S16872	cytochrome P450 2D
312	23	100.0	412	2	C86177	hypothetical prote	385	23	100.0	500	1	S37284	cytochrome P450 2D
313	23	100.0	412	2	F69796	sugar-binding, prot	386	23	100.0	502	2	C97640	probable ATP-depen
314	23	100.0	414	2	S24154	alanine-glyoxylate	387	23	100.0	502	2	AD2863	dead-box ATP-depen
315	23	100.0	414	2	T38742	hypothetical prote	388	23	100.0	503	2	AB2040	hypothetical prote
316	23	100.0	418	2	H83126	probable secretion	389	23	100.0	503	2	F95988	probable ATP-depen
317	23	100.0	420	2	AB0098	diaminopimelate de	390	23	100.0	504	1	A26822	debrisoquine 4-hyd
318	23	100.0	425	2	AB0813	hypothetical prote	391	23	100.0	504	1	A30247	cytochrome P450 2D
319	23	100.0	427	2	E87669	conserved hypotet	392	23	100.0	504	1	O4RTD5	cytochrome P450 2D
320	23	100.0	427	2	E96716	probable RNA-bindi	393	23	100.0	504	2	I49427	cytochrome P450 16
321	23	100.0	428	2	G82238	adenosylmethionine	394	23	100.0	505	2	A32261	agarase (EC 3.2.1.

395	23	100.0	507	2	T44312	hypothetical prote	468	23	100.0	638	2	T08917	auxin response fac
396	23	100.0	509	2	AH0578	citrate (pro-3S)-1	469	23	100.0	651	2	T11175	hypothetical prote
397	23	100.0	512	1	D70506	hypothetical prote	470	23	100.0	653	2	T48270	dnak-type molecula
398	23	100.0	517	2	A49413	perillipin A - rat	471	23	100.0	653	2	T48341	endoglin - mouse
399	23	100.0	527	1	T37895	hypothetical prote	472	23	100.0	655	2	S54183	acyl-CoA dehydroge
400	23	100.0	528	1	B70531	probable sigA prot	473	23	100.0	655	2	S44872	acyl-CoA dehydroge
401	23	100.0	529	2	B24059	t complex polypept	474	23	100.0	655	2	S40521	FKBP protein - hum
402	23	100.0	532	2	S74453	hypothetical prote	475	23	100.0	661	2	F83342	probable cation-tr
403	23	100.0	533	1	TVFVFP	protein-tyrosine k	476	23	100.0	661	2	E82414	biosynthetic argin
404	23	100.0	534	2	G75348	conserved hypothet	477	23	100.0	665	2	D96621	auxin response fac
405	23	100.0	534	2	S62572	hypothetical prote	478	23	100.0	665	2	S62328	kinesin-like DNA b
406	23	100.0	537	2	T50099	probable gamma-t	479	23	100.0	666	2	B70803	hypothetical prote
407	23	100.0	538	2	B83625	probable gamma-glu	480	23	100.0	668	2	C96501	hypothetical prote
408	23	100.0	546	2	D83408	hypothetical prote	481	23	100.0	670	2	C83540	conserved hypothet
409	23	100.0	548	1	HYBSS	bacillolysins (EC 3	482	23	100.0	673	2	A81936	hypothetical prote
410	23	100.0	551	2	S56283	protein-tyrosine-p	483	23	100.0	677	1	CNHUB	chromogranin B pre
411	23	100.0	553	2	T45872	hypothetical prote	484	23	100.0	677	2	S70722	hypothetical prote
412	23	100.0	555	2	T48453	hypothetical prote	485	23	100.0	678	2	S77215	hypothetical prote
413	23	100.0	556	2	S10486	t-complex-type mol	486	23	100.0	681	2	H83044	2,4-dienoyl-CoA re
414	23	100.0	556	2	S13163	t-complex-type mol	487	23	100.0	688	2	T32750	hypothetical prote
415	23	100.0	556	2	JH0475	t complex polypept	488	23	100.0	690	2	H84309	protoporphyrin IX
416	23	100.0	556	2	JC1443	t complex polypept	489	23	100.0	695	2	B75295	hypothetical prote
417	23	100.0	556	2	JQ0866	t complex protein	490	23	100.0	696	2	H90798	probable receptor
418	23	100.0	560	2	JCS180	serine C-palmitoyl	491	23	100.0	696	2	G85607	fused proteinase-c
419	23	100.0	565	2	T33851	thin filament-asso	492	23	100.0	697	2	JC2365	complement subcomp
420	23	100.0	567	2	JCS957	transforming growt	493	23	100.0	705	1	C1HURB	probable polyribon
421	23	100.0	571	2	T31170	maturase-related p	494	23	100.0	706	2	H81943	polyribonucleotide
422	23	100.0	574	2	H87036	RNA polymerase sig	495	23	100.0	707	2	C81161	hypothetical prote
423	23	100.0	574	2	AD1863	cobalamin biosynth	496	23	100.0	708	2	T48022	hypothetical prote
424	23	100.0	575	2	AG2566	hypothetical prote	497	23	100.0	710	2	T44753	hypothetical prote
425	23	100.0	579	2	JCS955	transforming growt	498	23	100.0	713	2	S27966	probable serine/th
426	23	100.0	592	2	T42078	serine/threonine p	499	23	100.0	715	2	T02836	long chain fatty a
427	23	100.0	597	2	T01808	hypothetical prote	500	23	100.0	716	1	WVQ53	80K protein - pola
428	23	100.0	599	2	JC8009	choline dehydrogen	501	23	100.0	718	2	A83282	probable TonB-depe
429	23	100.0	603	1	DNHUN5	NADH2 dehydrogenas	502	23	100.0	721	2	B83237	probable TonB-depe
430	23	100.0	603	2	B59154	NADH2 dehydrogenas	503	23	100.0	723	2	T14765	hypothetical prote
431	23	100.0	603	2	T11516	NADH2 dehydrogenas	504	23	100.0	727	2	JC7818	metalloproteinase
432	23	100.0	603	2	T14026	NADH2 dehydrogenas	505	23	100.0	728	1	JH0579	hepatocyte growth
433	23	100.0	603	2	T14149	NADH2 dehydrogenas	506	23	100.0	729	2	S76065	hypothetical prote
434	23	100.0	603	2	T14199	NADH2 dehydrogenas	507	23	100.0	732	2	T52588	wall-associated se
435	23	100.0	603	2	T11490	NADH2 dehydrogenas	508	23	100.0	733	2	A87168	conserved hypothet
436	23	100.0	603	2	JCS183	serine C-palmitoyl	509	23	100.0	739	2	I40715	malate synthase (E
437	23	100.0	603	2	T37518	probable transcrip	510	23	100.0	741	2	AF2297	hypothetical prote
438	23	100.0	604	2	T11867	NADH2 dehydrogenas	511	23	100.0	766	1	WZBEC5	infected cell prot
439	23	100.0	604	2	T11247	NADH2 dehydrogenas	512	23	100.0	766	2	H83141	probable two-compo
440	23	100.0	604	2	T36966	hypothetical prote	513	23	100.0	772	2	T13078	KIAA0992 protein -
441	23	100.0	605	2	A10551	maltodextrin gluco	514	23	100.0	774	1	QRECF4	iron(III) dicitrat
442	23	100.0	605	2	C64769	alpha-glucosidase	515	23	100.0	779	2	D82995	conserved hypothet
443	23	100.0	605	2	E90685	maltodextrin gluco	516	23	100.0	781	2	H95392	probable MrcB peni
444	23	100.0	605	2	A85536	maltodextrin gluco	517	23	100.0	782	2	S33945	late protein, 100K
445	23	100.0	606	1	QX805M	NADH2 dehydrogenas	518	23	100.0	784	2	H83158	Fe(III) dicitrate
446	23	100.0	606	2	T11503	NADH2 dehydrogenas	519	23	100.0	789	2	T28714	hypothetical prote
447	23	100.0	606	2	T11150	NADH2 dehydrogenas	520	23	100.0	790	2	E83621	probable TonB-depe
448	23	100.0	606	2	T11412	NADH2 dehydrogenas	521	23	100.0	791	2	T12455	hypothetical prote
449	23	100.0	606	2	S58851	NADH2 dehydrogenas	522	23	100.0	792	2	F83156	probable metal tra
450	23	100.0	606	2	C41830	NADH2 dehydrogenas	523	23	100.0	794	2	I58376	hypothetical prote
451	23	100.0	606	2	T45560	NADH2 dehydrogenas	524	23	100.0	795	2	D64343	hypothetical prote
452	23	100.0	606	2	T11373	NADH2 dehydrogenas	525	23	100.0	802	2	T45642	FtsH metalloprotei
453	23	100.0	606	2	T11257	NADH2 dehydrogenas	526	23	100.0	803	1	S35695	neurotrophin-3 rec
454	23	100.0	606	2	T11060	NADH2 dehydrogenas	527	23	100.0	815	2	B30843	glutenin high mole
455	23	100.0	606	2	S13526	hydrogenase (EC 1.	528	23	100.0	815	2	JN0689	glutenin, high-mol
456	23	100.0	606	2	JCS956	transforming growt	529	23	100.0	818	1	E64807	outer membrane ush
457	23	100.0	608	2	E84750	hypothetical prote	530	23	100.0	820	1	TVCTFF	protein-tyrosine k
458	23	100.0	608	2	T03278	gene ErtIN protein	531	23	100.0	821	2	B75530	ATP-dependent prot
459	23	100.0	608	2	G02640	polycystic kidney	532	23	100.0	824	2	I50618	c-fps proto oncoge
460	23	100.0	609	1	TMVVC	protein-tyrosine k	533	23	100.0	825	1	A40026	neurotrophin-3 rec
461	23	100.0	609	2	S26161	NADH2 dehydrogenas	534	23	100.0	825	2	A51178	neurotrophin recep
462	23	100.0	610	2	AD2632	NADH2 dehydrogenas	535	23	100.0	829	2	E87305	TonB-dependent rec
463	23	100.0	611	2	T04510	hypothetical prote	536	23	100.0	830	2	S15720	glutenin high mole
464	23	100.0	613	2	T47975	auxin response fac	537	23	100.0	832	2	E84543	probable beta-gala
465	23	100.0	614	2	S27962	modulator recognit	538	23	100.0	835	2	AH1861	DNA topoisomerase
466	23	100.0	616	2	I38231	S-laminin - human	539	23	100.0	836	2	T30312	pilin biosynthetic
467	23	100.0	622	2	A84904	hypothetical prote	540	23	100.0	839	1	I73632	neurotrophin-3 rec

541	23	100.0	846	2	S52418	GTP-binding regula	614	23	100.0	1333	2	A37488	Ras guanine nucleo
542	23	100.0	846	2	H70599	hypothetical prote	615	23	100.0	1336	2	S25716	Ras guanine nucleo
543	23	100.0	847	2	C87678	TonB-dependent rec	616	23	100.0	1350	2	S89756	protein T23E7.1 [i
544	23	100.0	848	2	S02262	glutenin high mole	617	23	100.0	1355	2	T28715	hypothetical prote
545	23	100.0	848	2	E86643	probable G-protein	618	23	100.0	1355	2	T00075	hypothetical prote
546	23	100.0	852	2	I51259	tyrosine kinase C	619	23	100.0	1369	2	S58160	hypothetical prote
547	23	100.0	855	2	C82983	hypothetical prote	620	23	100.0	1425	2	T30811	hepatocyte growth
548	23	100.0	872	2	H75564	probable ATP-depen	621	23	100.0	1438	2	T17402	dihydroaeruginosic
549	23	100.0	873	1	TVFVF	protein-tyrosine k	622	23	100.0	1468	2	F96610	probable polyprote
550	23	100.0	873	1	TVFVF	protein-tyrosine k	623	23	100.0	1503	2	T43166	alpha-2-macroglobu
551	23	100.0	880	1	E64113	DNA topoisomerase	624	23	100.0	1505	2	T43166	synaptonemal compl
552	23	100.0	885	2	I38968	100 kDa coactivato	625	23	100.0	1508	2	E87696	glutamate synthase
553	23	100.0	891	2	AF2915	cell division prot	626	23	100.0	1558	2	T29253	hypothetical prote
554	23	100.0	895	2	S20582	dystrophin-associa	627	23	100.0	1571	2	T00062	hypothetical prote
555	23	100.0	900	2	F71426	hypothetical prote	628	23	100.0	1736	2	T00391	hypothetical prote
556	23	100.0	902	2	A97690	cell division prot	629	23	100.0	1797	2	A55677	laminin beta-2 cha
557	23	100.0	916	2	S60779	DNA gyrase chain A	630	23	100.0	1798	2	S53869	laminin beta-2 cha
558	23	100.0	916	2	A81089	DNA gyrase chain A	631	23	100.0	1801	1	MMRTS	laminin beta-2 cha
559	23	100.0	923	2	H81853	DNA topoisomerase	632	23	100.0	1815	2	S73021	polyketide synthas
560	23	100.0	923	2	H83248	DNA gyrase subunit	633	23	100.0	1822	2	F87203	polyketide synthas
561	23	100.0	927	2	T51536	hypothetical prote	634	23	100.0	1827	2	B70984	probable polyketid
562	23	100.0	930	2	A25923	progesterone recep	635	23	100.0	1834	1	JDMU1	DNA-directed RNA p
563	23	100.0	943	2	G83448	2-oxoglutarate deh	636	23	100.0	1840	2	G85422	hypothetical prote
564	23	100.0	952	2	S32954	hypothetical prote	637	23	100.0	1896	1	RNFF2L	DNA-directed RNA p
565	23	100.0	965	2	C82560	excinuclease ABC c	638	23	100.0	2124	2	A28452	proteoglycan core
566	23	100.0	967	2	F82668	oxoglutarate dehyd	639	23	100.0	2139	2	T18296	myosin heavy chain
567	23	100.0	984	2	T44608	pyruvate carboxyla	640	23	100.0	2157	2	A13009	peptide synthetase
568	23	100.0	998	2	T30930	hypothetical prote	641	23	100.0	2199	2	T40008	Cdc20p - fission y
569	23	100.0	1003	2	A38234	oxoglutarate dehyd	642	23	100.0	2254	2	T09053	low voltage-activa
570	23	100.0	1006	2	T00050	hypothetical prote	643	23	100.0	2295	2	C88369	protein unc-52 [im
571	23	100.0	1006	2	F96683	hypothetical prote	644	23	100.0	2327	2	T42630	aggrscan - bovine
572	23	100.0	1023	2	G96509	protein F27F5.21 [645	23	100.0	2386	1	FNHU	fibronectin precur
573	23	100.0	1040	1	A38306	alpha-mannosidase	646	23	100.0	2437	2	S53611	MIB1 protein - ra
574	23	100.0	1044	2	T43155	nitrite reductase	647	23	100.0	2472	2	E83594	still frameshift p
575	23	100.0	1044	2	T43155	nitrite reductase	648	23	100.0	2491	1	A28372	insulin-like growt
576	23	100.0	1051	2	C95367	conserved hypothet	649	23	100.0	2566	2	E98274	hypothetical prote
577	23	100.0	1054	2	A61221	probable calcium t	650	23	100.0	2723	2	T03221	probable polyketid
578	23	100.0	1056	2	A53767	mucin MUC5B, trach	651	23	100.0	2767	1	UIHU	thyroglobulin prec
579	23	100.0	1072	2	A84112	alkaline amylopull	652	23	100.0	2796	2	JC4743	faty-acid synthas
580	23	100.0	1075	2	T31668	hypothetical prote	653	23	100.0	2899	2	T21546	hypothetical prote
581	23	100.0	1076	2	T31668	nccA protein - Aic	654	23	100.0	2915	2	G87867	protein F36A2.13 [
582	23	100.0	1090	2	A41696	regulatory protein	655	23	100.0	3175	1	RRWVEV	genome polyprotein
583	23	100.0	1097	2	D70612	probable recC prot	656	23	100.0	3375	2	T19821	hypothetical prote
584	23	100.0	1100	2	G83376	probable trehalose	657	23	100.0	3566	1	A40701	tenascin-X precurs
585	23	100.0	1122	1	NCECVV	exodeoxyribonuclea	658	23	100.0	3942	2	T42730	Bassoon protein -
586	23	100.0	1122	2	G91088	DNA helicase RecC	659	23	100.0	4006	2	T09070	probable tenascin
587	23	100.0	1122	2	A85934	DNA helicase RecC	660	23	100.0	4135	2	T42629	tenascin-X - bovin
588	23	100.0	1122	2	T14180	exit protein - Myc	661	23	100.0	4910	2	S64942	probable membrane
589	23	100.0	1123	2	AD0865	exonuclease V chai	662	23	100.0	5147	1	IJFFTM	cadherin-related t
590	23	100.0	1123	2	AB0125	dynamin heavy chain	663	23	100.0	7463	2	T36248	CDA peptide synthe
591	23	100.0	1123	2	T30880	pyruvate carboxyla	664	20	87.0	8	2	PT0691	T-cell receptor be
592	23	100.0	1146	2	AH1208	pyruvate carboxyla	665	20	87.0	26	2	S14035	hypothetical prote
593	23	100.0	1146	2	AC1565	pyruvate carboxyla	666	20	87.0	26	2	S14036	hypothetical prote
594	23	100.0	1148	2	F69685	pyruvate carboxyla	667	20	87.0	26	2	S14037	hypothetical prote
595	23	100.0	1150	2	A83978	pyruvate carboxyla	668	20	87.0	29	2	A39462	cholesterolin - do
596	23	100.0	1151	2	A45226	integrin alpha-1 c	669	20	87.0	31	2	I54515	pre-B cell Ig lamb
597	23	100.0	1155	2	T39040	hypothetical prote	670	20	87.0	34	2	F82394	hypothetical prote
598	23	100.0	1158	2	AE3285	pyruvate carboxyla	671	20	87.0	37	2	I56058	cell surface glyco
599	23	100.0	1162	2	AD3317	carbamoyl-phosphat	672	20	87.0	40	2	PQ0533	3-oxoacyl-l-acyl-ca
600	23	100.0	1171	2	T05039	hypothetical prote	673	20	87.0	53	2	S41957	naringenin-chalcon
601	23	100.0	1174	2	AE2911	pyruvate carboxyla	674	20	87.0	60	2	AD2783	hypothetical prote
602	23	100.0	1174	2	C97686	pyruvate carboxyla	675	20	87.0	60	2	E97562	hypothetical prote
603	23	100.0	1180	2	A35854	integrin alpha-1 c	676	20	87.0	63	1	GCIDC	glucagon precursor
604	23	100.0	1199	2	T29145	hypothetical prote	677	20	87.0	63	2	G69073	rubredoxin - Metha
605	23	100.0	1207	2	T00378	KIAA0641 protein	678	20	87.0	65	2	S51099	MHC class I histoc
606	23	100.0	1208	2	T00362	hypothetical prote	679	20	87.0	65	2	D84209	hypothetical prote
607	23	100.0	1236	2	S68700	HPTP beta-like tyr	680	20	87.0	65	2	B25103	ferredoxin 2[4Fe-4
608	23	100.0	1260	2	A72603	probable nitrate r	681	20	87.0	65	2	B35405	ferredoxin 2[4Fe-4
609	23	100.0	1289	2	B70748	probable smc prote	682	20	87.0	66	2	T35489	hypothetical prote
610	23	100.0	1298	1	EDBE75	immediate-early pr	683	20	87.0	71	2	A40962	cAMP-dependent pro
611	23	100.0	1313	2	T29193	hypothetical prote	684	20	87.0	71	2	E83054	hypothetical prote
612	23	100.0	1317	2	T03748	apoptosis associat	685	20	87.0	72	2	E82615	hypothetical prote
613	23	100.0	1321	2	JE0352	mucin MUC5B, trach	686	20	87.0	75	2	S61573	probable membrane

687	20	87.0	76	2	T40983	hypothetical prote	760	134	2	A70315	AP4A hydrolase -	
688	20	87.0	76	2	T45326	hypothetical prote	761	134	2	PC4214	phosphatidylethane	
689	20	87.0	80	2	F83602	conserved hypotet	762	134	2	B87632	hypothetical prote	
690	20	87.0	82	2	F96625	hypothetical prote	763	136	2	S16848	Ig lambda chain V-	
691	20	87.0	83	2	T35070	probable membrane	764	20	87.0	137	S68429	myotoxin precursor
692	20	87.0	85	2	A87006	hypothetical prote	765	20	87.0	138	I50098	phospholipase A2 -
693	20	87.0	85	2	T50340	hypothetical prote	766	20	87.0	138	S67968	transition protein
694	20	87.0	86	2	T17313	hypothetical prote	767	20	87.0	139	H87488	lactoylglutathione
695	20	87.0	87	2	S52290	HLA-A30 variant ex	768	20	87.0	139	AF0685	hypothetical prote
696	20	87.0	88	2	B42175	tenascin homolog 3	769	20	87.0	140	PH0132	Ig lambda chain pr
697	20	87.0	89	2	G71378	hypothetical prote	770	20	87.0	140	PH0134	Ig lambda chain pr
698	20	87.0	91	2	S06351	excisionase - phag	771	20	87.0	140	H96923	transcription regu
699	20	87.0	91	2	H75613	conserved hypotet	772	20	87.0	141	S40768	hypothetical prote
700	20	87.0	92	2	B46707	CAMP-dependent pro	773	20	87.0	141	A70556	probable mutator M
701	20	87.0	97	2	JT0703	ferredoxin-thiore	774	20	87.0	143	JQ0425	hypothetical 15.5K
702	20	87.0	98	2	I40888	sarcosine oxidase	775	20	87.0	144	I70695	omega protein - hu
703	20	87.0	100	2	F69133	ribosomal protein	776	20	87.0	145	S25743	Ig lambda chain -
704	20	87.0	102	2	B83314	hypothetical prote	777	20	87.0	147	AB0900	conserved hypotet
705	20	87.0	105	2	S22762	Ig lambda-2 chain	778	20	87.0	147	F85978	hypothetical prote
706	20	87.0	105	2	B27390	Ig lambda-2 chain	779	20	87.0	147	C91133	hypothetical prote
707	20	87.0	105	2	S22759	Ig lambda-2 chain	780	20	87.0	147	F65105	hypothetical prote
708	20	87.0	106	2	S00259	Ig lambda-5 chain	781	20	87.0	147	JX0261	phospholipase A2 i
709	20	87.0	106	2	S22760	Ig lambda-2 chain	782	20	87.0	149	S23626	Ig lambda chain V
710	20	87.0	106	2	AC3086	sarcosine oxidase	783	20	87.0	149	S47574	BtT1 protein - yea
711	20	87.0	106	2	F98200	sarcosine oxidase	784	20	87.0	150	C98254	probable acyl-CoA
712	20	87.0	106	2	H87560	conserved hypotet	785	20	87.0	150	S26068	hypothetical prote
713	20	87.0	107	2	T17856	hypothetical prote	786	20	87.0	151	S25739	Ig lambda chain -
714	20	87.0	108	2	T29957	hypothetical prote	787	20	87.0	151	F95942	hypothetical prote
715	20	87.0	109	2	F25546	hypothetical prote	788	20	87.0	151	F72806	gp55 protein - Myc
716	20	87.0	112	2	AB3507	phosphoribosyl-ATP	789	20	87.0	152	F86473	hypothetical prote
717	20	87.0	112	2	C72679	hypothetical prote	790	20	87.0	152	S76383	hypothetical prote
718	20	87.0	113	2	A29700	Ig lambda chain V	791	20	87.0	154	1 XMECF1	flagellar protein
719	20	87.0	113	2	B54256	Ig lambda-1 chain	792	20	87.0	154	C90964	flagellar protein
720	20	87.0	114	2	PH0133	Ig lambda chain V	793	20	87.0	154	C85812	flagellar biosynth
721	20	87.0	114	2	T49338	hypothetical prote	794	20	87.0	155	AH0752	FlilL protein limpo
722	20	87.0	118	2	S12442	Ig lambda chain (K	795	20	87.0	155	B30929	flagellar protein
723	20	87.0	118	2	S12441	Ig lambda chain (K	796	20	87.0	155	H75075	hypothetical prote
724	20	87.0	118	2	S12440	Ig lambda chain (M	797	20	87.0	158	E86993	hypothetical prote
725	20	87.0	118	2	S12443	Ig lambda chain (K	798	20	87.0	160	E86365	ripening-induced p
726	20	87.0	118	2	A39949	Ig lambda chain J-	799	20	87.0	160	A10760	probable propanedi
727	20	87.0	119	2	S30526	Ig lambda chain J-	800	20	87.0	161	C84235	hypothetical prote
728	20	87.0	119	2	S03465	Ig lambda chain J-	801	20	87.0	162	E87509	conserved hypotet
729	20	87.0	120	2	S30528	Ig lambda chain V	802	20	87.0	165	AB2721	N-utilization subs
730	20	87.0	120	2	S30527	Ig lambda chain V	803	20	87.0	166	I69004	histocompatibility
731	20	87.0	120	2	S30525	Ig lambda chain V	804	20	87.0	166	AH2568	hypothetical prote
732	20	87.0	120	2	B90158	conserved hypotet	805	20	87.0	168	H90588	hypothetical prote
733	20	87.0	120	2	D83166	hypothetical prote	806	20	87.0	168	T45305	hypothetical prote
734	20	87.0	120	2	JC4754	hypothetical 13.6k	807	20	87.0	169	F97502	nusb protein (PA40
735	20	87.0	120	2	T34431	hypothetical prote	808	20	87.0	171	T49789	hypothetical prote
736	20	87.0	121	1	PSBGAC	phospholipase A2 (809	20	87.0	171	C81280	probable periplasm
737	20	87.0	121	1	PS8NAM	phospholipase A2 h	810	20	87.0	172	F83585	probable sigma-70
738	20	87.0	122	2	S93114	phospholipase A2 (811	20	87.0	174	H96001	hypothetical prote
739	20	87.0	122	2	S29882	ribosomal protein	812	20	87.0	175	C75300	hypothetical prote
740	20	87.0	122	2	E85751	hypothetical prote	813	20	87.0	175	C72513	hypothetical prote
741	20	87.0	122	2	D90867	hypothetical prote	814	20	87.0	176	T46479	hypothetical prote
742	20	87.0	123	2	A53335	Na+/Ca2+-exchangin	815	20	87.0	176	F88535	protein B0523.3 [i
743	20	87.0	123	2	I46959	Na/Ca exchanger NA	816	20	87.0	179	A75019	hypothetical prote
744	20	87.0	123	2	AH2667	conserved hypotet	817	20	87.0	179	C71205	hypothetical prote
745	20	87.0	123	2	E97449	hypothetical prote	818	20	87.0	181	PT0220	Ig lambda chain V-
746	20	87.0	124	2	S25113	insulin-like growt	819	20	87.0	181	I79640	MHC cell surface a
747	20	87.0	124	2	D84319	30S ribosomal prot	820	20	87.0	181	I59188	MHC cell surface g
748	20	87.0	126	2	AG1125	B. subtilis YyAH p	821	20	87.0	182	A49411	human leukocyte an
749	20	87.0	128	2	S33611	naringenin-chalcon	822	20	87.0	183	G83642	DNA-3-methyladenin
750	20	87.0	128	2	QJ1203	hypothetical 14K p	823	20	87.0	184	F75481	hypothetical prote
751	20	87.0	128	2	C90436	conserved hypotet	824	20	87.0	185	F70479	flavodoxin - Aquif
752	20	87.0	128	2	H96614	probable myrosinas	825	20	87.0	187	AH0114	conserved hypotet
753	20	87.0	129	2	AH3031	acyl-CoA hydrolase	826	20	87.0	187	S87299	hypothetical prote
754	20	87.0	131	2	F72236	hypothetical prote	827	20	87.0	187	S63461	hypothetical prote
755	20	87.0	132	1	T43826	ribosomal protein	828	20	87.0	189	1 A69024	conserved hypotet
756	20	87.0	132	2	T38486	probable ribosomal	829	20	87.0	189	2 S95418	probable kdpC pota
757	20	87.0	132	2	B69489	LSU ribosomal prot	830	20	87.0	190	2 S25740	Ig lambda chain -
758	20	87.0	132	2	F84322	50S ribosomal prot	831	20	87.0	190	2 AC0619	hypothetical bacte
759	20	87.0	134	2	A75535	ribosomal protein	832	20	87.0	192	2 AF1876	hypothetical prote

833	20	87.0	193	2	E82171	DNA-3-methyladenin	906	20	87.0	233	2	S25748	Ig lambda chain -
834	20	87.0	193	2	AF1823	hypothetical prote	907	20	87.0	233	2	S25752	Ig lambda chain -
835	20	87.0	195	2	T43227	hypothetical prote	908	20	87.0	233	2	AC0463	high-affinity bran
836	20	87.0	195	2	B56688	molybdopterin bios	909	20	87.0	233	2	T35594	hypothetical prote
837	20	87.0	195	2	A85481	molybdopterin bio	910	20	87.0	233	2	F64482	hypothetical prote
838	20	87.0	195	2	A90630	molybdopterin bios	911	20	87.0	234	2	S25757	Ig lambda chain -
839	20	87.0	195	2	AE0057	molybdopterin bios	912	20	87.0	234	2	A39956	Ig lambda chain pr
840	20	87.0	196	2	AI0502	molybdopterin bios	913	20	87.0	234	2	T21495	hypothetical prote
841	20	87.0	197	2	D64148	molybdopterin bios	914	20	87.0	235	2	S05270	Ig lambda chain pr
842	20	87.0	197	2	S44735	b0523.3 protein -	915	20	87.0	235	2	S25754	Ig lambda chain -
843	20	87.0	199	2	T06871	endopeptidase Clp	916	20	87.0	235	2	S25759	Ig lambda chain -
844	20	87.0	201	2	B70416	endopeptidase Clp	917	20	87.0	235	2	S25750	Ig lambda chain -
845	20	87.0	201	2	A31484	troponin I, fast s	918	20	87.0	235	2	S25749	Ig lambda chain -
846	20	87.0	202	2	C72701	probable heme expo	919	20	87.0	235	2	S25758	Ig lambda chain -
847	20	87.0	203	2	T30493	hypothetical prote	920	20	87.0	235	2	S14675	Ig lambda chain -
848	20	87.0	203	2	AI0367	probable lipoprote	921	20	87.0	236	2	S25746	Ig lambda chain -
849	20	87.0	204	2	T25709	hypothetical prote	922	20	87.0	236	2	F63128	Ig lambda chain -
850	20	87.0	204	2	F87295	conserved hypotet	923	20	87.0	237	2	D87373	hypothetical prote
851	20	87.0	205	2	C95131	hypothetical prote	924	20	87.0	237	2	T10629	hypothetical prote
852	20	87.0	205	2	G87370	peptidyl-prolyl ci	925	20	87.0	238	2	T73858	arginine deiminase
853	20	87.0	206	2	I37529	HLA-Cw7 - human (f	926	20	87.0	239	2	T39885	hypothetical prote
854	20	87.0	206	2	I37528	HLA-Cw1 - human (f	927	20	87.0	240	2	T27629	hypothetical prote
855	20	87.0	206	2	JI0059	H-2 class I histoc	928	20	87.0	241	2	S25435	chlorophyll a/b-bi
856	20	87.0	206	2	JLC058	H-2 class I histoc	929	20	87.0	241	2	D87337	ada regulatory pro
857	20	87.0	206	2	JC7320	K562 cell-derived	930	20	87.0	242	2	D95217	choline transporte
858	20	87.0	208	2	T43385	60S ribosomal prot	931	20	87.0	242	2	A72706	hypothetical prote
859	20	87.0	208	2	T17343	hypothetical prote	932	20	87.0	242	2	D98081	hypothetical prote
860	20	87.0	209	1	A26166	Ig lambda-5 chain	933	20	87.0	243	2	S25755	Ig lambda chain -
861	20	87.0	209	2	H82561	hypothetical prote	934	20	87.0	243	2	I54459	MHC H-2K1-k - mous
862	20	87.0	210	2	T05298	hypothetical prote	935	20	87.0	244	2	B75459	sodium extrusion p
863	20	87.0	211	2	C87462	hypothetical prote	936	20	87.0	247	1	LNRBPS	pulmonary surfacta
864	20	87.0	213	2	A21177	Ig light chain pre	937	20	87.0	247	2	D72332	conserved hypotet
865	20	87.0	213	2	PC21066	Ig lambda chain V	938	20	87.0	248	1	LNDGPS	pulmonary surfacta
866	20	87.0	214	2	SQ4156	Ig lambda chain V	939	20	87.0	248	1	LNRTPS	pulmonary surfacta
867	20	87.0	214	2	D84808	hypothetical prote	940	20	87.0	248	2	A48853	pulmonary surfacta
868	20	87.0	214	2	H75592	conserved hypotet	941	20	87.0	248	2	T35233	hypothetical prote
869	20	87.0	215	2	T49743	probable rrm-type	942	20	87.0	249	2	H90741	molybdopterin bios
870	20	87.0	216	2	A42193	Ig lambda chain (B	943	20	87.0	249	2	AI0602	molybdopterin bios
871	20	87.0	216	2	S03401	Ig lambda chain (K	944	20	87.0	249	2	C85592	molybdopterin bios
872	20	87.0	216	2	S69130	Ig lambda chain (D	945	20	87.0	249	2	B32352	molybdopterin bios
873	20	87.0	216	2	JE0241	Ig kappa chain AmJ	946	20	87.0	249	2	S07917	molybdopterin bios
874	20	87.0	216	2	S29258	Ig lambda chain V	947	20	87.0	249	2	H90048	hypothetical prote
875	20	87.0	217	2	F75627	potassium-transport	948	20	87.0	249	2	S76552	hypothetical prote
876	20	87.0	217	2	T50004	rRNA binding protei	949	20	87.0	250	2	E75376	2-hydroxyhepta-2,4
877	20	87.0	218	2	D87264	hypothetical prote	950	20	87.0	250	2	H75504	MutT/nudix family
878	20	87.0	220	2	D87535	glutathione S-tran	951	20	87.0	251	1	S35729	myb-related protei
879	20	87.0	220	2	F65218	conserved hypotet	952	20	87.0	252	2	B82181	oxidoreductase, sh
880	20	87.0	221	1	JN0489	butyrate-acetoacet	953	20	87.0	253	2	C84177	proteasome, subuni
881	20	87.0	221	2	AF3379	molybdopterin-guan	954	20	87.0	253	2	AE2021	hypothetical prote
882	20	87.0	222	2	HA2619	conserved hypotet	955	20	87.0	254	2	F83271	hypothetical prote
883	20	87.0	222	2	H97401	probable endopepti	956	20	87.0	255	2	I54307	hypothetical prote
884	20	87.0	223	2	H87335	conserved hypotet	957	20	87.0	255	2	C90431	MHC HLA-A30J3 heav
885	20	87.0	224	1	S76529	hypothetical prote	958	20	87.0	255	2	S12255	conserved hypotet
886	20	87.0	224	2	B87440	transcription regu	959	20	87.0	256	2	B95383	hypothetical prote
887	20	87.0	225	1	A64181	nrfC protein - Hae	960	20	87.0	256	2	AH1978	probable Short Cha
888	20	87.0	225	2	T36651	probable cation tr	961	20	87.0	259	2	AD3141	hypothetical prote
889	20	87.0	226	2	S25745	Ig lambda chain -	962	20	87.0	259	2	H98146	probable amino-aci
890	20	87.0	226	2	T06651	hypothetical prote	963	20	87.0	259	2	C90754	hypothetical prote
891	20	87.0	230	2	S94449	Ig lambda chain -	964	20	87.0	259	2	G64831	probable membrane
892	20	87.0	230	2	A70821	hypothetical prote	965	20	87.0	259	2	A85618	hypothetical prote
893	20	87.0	231	2	S26035	cytochrome-c oxida	966	20	87.0	260	2	A84695	probable tropinone
894	20	87.0	231	2	S25751	Ig lambda chain -	967	20	87.0	260	2	D86266	hypothetical prote
895	20	87.0	231	2	S25738	Ig lambda chain -	968	20	87.0	261	2	G70980	transcription inic
896	20	87.0	232	2	S26023	cytochrome-c oxida	969	20	87.0	262	2	F72336	conserved hypotet
897	20	87.0	232	2	S25742	Ig lambda chain -	970	20	87.0	262	2	E75400	hypothetical prote
898	20	87.0	232	2	S25756	Ig lambda chain -	971	20	87.0	262	2	T27848	hypothetical prote
899	20	87.0	232	2	D75062	probable flagella-	972	20	87.0	263	1	S23009	insulin-like growt
900	20	87.0	232	2	JQ0886	hypothetical prote	973	20	87.0	264	2	T46335	hypothetical prote
901	20	87.0	232	2	C72609	hypothetical prote	974	20	87.0	265	2	AB2453	molybdate-binding
902	20	87.0	232	2	H71169	hypothetical prote	975	20	87.0	265	2	T35512	hypothetical prote
903	20	87.0	233	2	B61222	cytochrome-c oxida	976	20	87.0	265	2	T15486	hypothetical prote
904	20	87.0	233	2	S25744	Ig lambda chain -	977	20	87.0	266	1	A35037	insulin-like growt
905	20	87.0	233	2	S25747	Ig lambda chain -	978	20	87.0	266	2	G87527	peptidase, M23/M37

979 20 87.0 267 2 A75131
 980 20 87.0 268 2 A71087
 981 20 87.0 269 2 T36360
 982 20 87.0 269 2 AF3494
 983 20 87.0 269 2 AG2268
 984 20 87.0 269 2 S22781
 985 20 87.0 270 1 HLUH28
 986 20 87.0 270 1 S77085
 987 20 87.0 270 2 AC1956
 988 20 87.0 272 1 A36082
 989 20 87.0 272 2 I48600
 990 20 87.0 272 2 B22826
 991 20 87.0 273 1 HLUHAW
 992 20 87.0 273 1 HLUH69
 993 20 87.0 273 2 I38509
 994 20 87.0 273 2 B64446
 995 20 87.0 273 2 C97222
 996 20 87.0 274 1 HLUH32
 997 20 87.0 274 2 I68774
 998 20 87.0 274 2 I54463
 999 20 87.0 274 2 S24439
 1000 20 87.0 274 2 AI0643

ALIGNMENTS

RESULT 1
 F70540
 Hypoetical protein Rv1572c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: F70540
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:198295987; PMID:9634230
 A:Accession: F70540
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-27 <COL>
 A:Cross-references: UNIPROT:O06618; GB:Z95586; GB:AL123456; NID:G3261785; PIDN:CAB09065.
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv1572c

Query Match 100.0%; Score 23; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 2 GQPR 5

RESULT 2
 F98129
 Hypoetical protein AGR_L18 [imported] - Agrobacterium tumefaciens (strain C58, Cerson
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: F98129
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: F98129
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <KUR>

A:Cross-references: UNIPROT:Q8U521; GB:AE007870; PIDN:AAK88560.1; PID:gl15158269; GSPDB:G
 C:Genetics:
 A:Gene: AGR_L18
 A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 9 GQPR 12

RESULT 3
 AE2406
 Hypoetical protein asl4805 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE2406
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shampo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2406
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-65 <KUR>
 A:Cross-references: UNIPROT:Q8YMW9; GB:BA000019; PIDN:BA076504.1; PID:gl17133942; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asl4805

Query Match 100.0%; Score 23; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 27 GQPR 30

RESULT 4
 F84040
 Hypoetical protein BH3126 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: F84040
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: F84040
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-67 <STO>
 A:Cross-references: UNIPROT:Q9K980; GB:AP001517; GB:BA000004; NID:gl0175500; PIDN:BA0684
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3126

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 58 GQPR 61

RESULT 5

T51191
small zinc finger-like protein [imported] - human
C:Species: Homo sapiens (man)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51191
R:Bauer, M.F.; Brunner, M.; Hofmann, S.
submitted to the EMBL Data Library, May 1999
A:Description: Cloning and mapping of the Tim10/DDP gene family encoding small zinc finger protein
A:Reference number: Z25334
A:Accession: T51191
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <BAU>
A:Cross-references: UNIPROT:Q9Y5J7; EMBL:AF150100; PIDN:AAD40006.1
C:Genetics:
A:Gene: TIM9a

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 86 GQPR 89

RESULT 6
T51192
small zinc finger-like protein [imported] - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51192
R:Bauer, M.F.; Brunner, M.; Hofmann, S.
submitted to the EMBL Data Library, May 1999
A:Description: Cloning and mapping of the Tim10/DDP gene family encoding small zinc finger protein
A:Reference number: Z25334
A:Accession: T51192
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <BAU>
A:Cross-references: UNIPROT:Q9WV98; EMBL:AF150101; PIDN:AAD40007.1
C:Genetics:
A:Gene: Tim9a

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 86 GQPR 89

RESULT 7
AD0847
hydrogenase isoenzymes formation protein HycC [imported] - Salmonella enterica subsp. en
C:Species: salmonella enterica subsp. enterica serovar Typhi
C>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 14-Apr-2003
C:Accession: AD0847
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0847
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05963.1; PID:g16503934; GSPDB:GN00176
C:Genetics:

A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 8
S15199
hydrogenase expression/formation protein hycC - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S15199; D65053
R:Rut, S.; Jacobi, A.; Schlensog, V.; Boehm, R.; Sawers, G.; Boeck, A.
Mol. Microbiol. 5, 123-135, 1991
A>Title: Molecular characterization of an operon (hyc) necessary for the activity of the
A:Reference number: S15197; MUID:91194542; PMID:1849603
A:Accession: S15199
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <LUT>
A:Cross-references: UNIPROT:P24191; EMBL:X54543; NID:g41774; PIDN:CAA38414.1; PID:g41777
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D65053
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <BLAT>
A:Cross-references: GB:AE000356; GB:U00096; NID:g2367153; PIDN:AACT5770.1; PID:g1789083;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 9
H85921
pleiotropic effects on 3 hydrogenase isozymes [imported] - Escherichia coli (strain O15:
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85921
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPROT:P24191; GB:AE005174; NID:g12517180; PIDN:AAG57836.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;

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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 40 GQPR 43

RESULT 10
H91076
hydrogenase isoenzyme HycC [imported] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H91076
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinsagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; PMID:11258796
A:Accession: H91076
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HAY>
A:Cross-references: UNIPROT:P24191; GB:BA000007; PIDN:BA837007.1; PID:g13363055; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
C:Gene: EC83584
C:Superfamily: [NifH]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 40 GQPR 43

RESULT 11
AG2217
hypothetical protein asr3294 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
C:Accession: AG2217
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; PMID:11759840
A:Accession: AG2217
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <KUR>
A:Cross-references: UNIPROT:Q8YR28; GB:BA000019; PIDN:BA874993.1; PID:g17132389; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: asr3294
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 100.0%; Score 23; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 51 GQPR 54

RESULT 12
D72601
hypothetical protein APES047 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix

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C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D72601
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; PMID:99310339; PMID:10382966
A:Accession: D72601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KAW>
A:Cross-references: UNIPROT:Q9YCI1; DDBJ:AP0000061; NID:g5104821; PIDN:BAA80266.1; PID:d1
A:Experimental source: strain K1
C:Genetics:
C:Gene: APES047
C:Superfamily: phosphoesterase, MJ0912 type; phosphoesterase core homology

Query Match 100.0%; Score 23; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 25 GQPR 28

RESULT 13
G97567
hypothetical protein AGR_C_3166 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97567
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: G97567
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: UNIPROT:Q8UEN1; GB:AE007869; PIDN:AAK87496.1; PID:g15156823; GSPDB:G
C:Genetics:
C:Gene: AGR_C_3166
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 45 GQPR 48

RESULT 14
AF2788
hypothetical protein Atul725 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2788
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AF2788
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>

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A;Cross-references: UNIPROT:QBUEN1; GB:AE008688; PIDN:AAL42724.1; PID:gl7740163; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul725
A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 45 GQPR 48

RESULT 15
F75500
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75500
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <WHI>
A;Cross-references: UNIPROT:Q9RW85; GB:AE001917; GB:AE000513; NID:g6458281; PIDN:AAF1017
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0590
A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 54 GQPR 57

RESULT 16
S19733
hypothetical protein 2 - Thiobacillus versutus (fragment)
C;Species: Thiobacillus versutus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S19733
R;Ubbink, M.; van Kleef, M.A.G.; Kleinjan, D.J.; Holtink, C.W.G.; Huitema, F.; Beintema,
Eur. J. Biochem. 202, 1003-1012, 1991
A;Title: Cloning, sequencing and expression studies of the genes encoding amicyanin and
A;Reference number: S19730; MUID:92111471; PMID:1765062
A;Accession: S19733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <UBB>
A;Cross-references: UNIPROT:Q56464; GB:M58001; NID:gl54632; PIDN:AAA50572.1; PID:gl54636

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 27 GQPR 30

RESULT 17
I39621
vpr protein - human immunodeficiency virus type 2 (isolate ST)
N;Alternate names: orf-R protein
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: E33943
R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.;
J. Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A;Reference number: A33943; MUID:90112862; PMID:2296086
A;Accession: E33943
A;Molecule type: genomic RNA
A;Residues: 1-104 <KUM>

rbpA1 protein - Anabaena variabilis
C;Species: Anabaena variabilis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 16-Aug-2004
C;Accession: I39621
R;Sato, N.
Plant Mol. Biol. 24, 819-823, 1994
A;Title: A cold-regulated cyanobacterial gene cluster encodes RNA-binding protein and rlt
A;Reference number: I39620; MUID:94250845; PMID:8193307
A;Accession: I39621
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-102 <RES>
A;Cross-references: UNIPROT:Q44560; GB:D17710; NID:g600249; PIDN:BAA04563.1; PID:g532033
C;Genetics:
A;Gene: rbpA1
C;Superfamily: ribonucleoprotein repeat homology
F;2-69/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 39 GQPR 42

RESULT 18
AC1899
RNA-binding protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC1899
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anac
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1899
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <KUR>
A;Cross-references: UNIPROT:Q44560; GB:BA000019; PIDN:BA072698.1; PID:gl7130086; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: rbpA1
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 39 GQPR 42

RESULT 19
ASLJSY
vpr protein - human immunodeficiency virus type 2 (isolate ST)
N;Alternate names: orf-R protein
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: E33943
R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.;
J. Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A;Reference number: A33943; MUID:90112862; PMID:2296086
A;Accession: E33943
A;Molecule type: genomic RNA
A;Residues: 1-104 <KUM>

A;Cross-references: UNIPROT:P20884; GB:M31113; NID:gl339798; PIDN:AAB01355.1; PID:g32575
 C;Genetics:
 A;Gene: vpr
 C;Superfamily: AIDS vpr protein
 C;Keywords: AIDS; immunodeficiency

Query Match 100.0%; Score 23; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 86 GQPR 89

RESULT 20
 G84541
 hypothetical protein At2g16590 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G84541
 R;Bin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: G84541
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-106 <STO>
 A;Cross-references: UNIPROT:Q9SI59; GB:AE002093; NID:g4589971; PIDN:AAD26488.1; GSPDB:GN
 C;Genetics:
 A;Gene: At2g16590
 A;Map position: 2

Query Match 100.0%; Score 23; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 55 GQPR 58

RESULT 21
 H72687
 hypothetical protein APE0920 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: H72687
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: H72687
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <KAW>
 A;Cross-references: UNIPROT:Q9YDU3; DDBJ:AP000060; NID:g5104188; PIDN:BAA79904.1; PID:dl
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0920
 C;Superfamily: Aeropyrum pernix hypothetical protein APE0920

Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 24 GQPR 27

RESULT 22

C83432
 conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aer
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: C83432
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: C83432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <STO>
 A;Cross-references: UNIPROT:Q9I328; GB:AE004597; GB:AE004091; NID:g9947671; PIDN:AAG05091
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA1702

Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 22 GQPR 25

RESULT 23

T46397
 hypothetical protein DKFZp434K0920.1 - human
 C;Species: Homo sapiens (man)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T46397
 R;Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23031
 A;Accession: T46397
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-115 <AAA>
 A;Cross-references: UNIPROT:Q9NTJ7; EMBL:AL136802
 A;Experimental source: adult testis; clone DKFZp434K0920
 C;Genetics:
 A;Note: DKFZp434K0920.1

Query Match 100.0%; Score 23; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 105 GQPR 108

RESULT 24

AG0688
 probable bacteriophage baseplate protein STY1634 [imported] - Salmonella enterica subsp.
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 C;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AG0688
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 , S.; Moulie, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AG0688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD01880.1; PID:g16502723; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1634

Query Match 100.0%; Score 23; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 105 GQPR 108

RESULT 25
 S14079
 pin1 protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S14079
 R:Saris, C.J.M.; Domen, J.; Berns, A.
 EMBO J. 10, 655-664, 1991
 A:Title: The pin-1 oncogene encodes two related protein-serine/threonine kinases by alternative splicing
 A:Reference number: S14079; MUID:91160521; PMID:1825810
 A:Accession: S14079
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-118 <SAR>

Query Match 100.0%; Score 23; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 51 GQPR 54

RESULT 26
 E75464
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: E75464
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75464
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-122 <WHI>
 A:Cross-references: UNIPROT:Q9RV21; GB:AE001941; GB:AE000513; NID:g6458589; PIDN:AAF1046
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0879
 A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 35 GQPR 38

RESULT 27

H95343
 hypothetical protein Sma1201 [imported] - Sinorhizobium meliloti (strain 1021) magaplaasm
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: H95343
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: H95343
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <KUR>
 A:Cross-references: UNIPROT:Q92241; GB:AE006469; PIDN:AAK65314.1; PID:g14523770; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler, pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma1201
 A:Gene: plasmid

Query Match 100.0%; Score 23; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 31 GQPR 34

RESULT 28
 A98346
 hypothetical protein AGR_L_3432 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: A98346
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: A98346
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-128 <KUR>
 A:Cross-references: UNIPROT:Q8URC4; GB:AE007870; PIDN:AAK90291.1; PID:g15160318; GSPDB:G
 C:Genetics:
 A:Gene: AGR_L_3432
 A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 27 GQPR 30

RESULT 29
 H81809
 hypothetical protein NMA1835 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: H81809

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <PAR>
A:Cross-references: UNIPROT:Q9JQNS; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB8506
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1835

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 64 GQPR 67

RESULT 30
C87219
hypothetical protein [imported] - *Mycobacterium leprae*
C:Species: *Mycobacterium leprae*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87219
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: C87219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <STO>
A:Cross-references: UNIPROT:Q9CB30; GB:AL450380; NID:G13094034; PIDN:CAC31995.1; GSPDB:G
C:Genetics:
A:Gene: ML2478

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 45 GQPR 48

RESULT 31
G70667
hypothetical protein Rv1871c - *Mycobacterium tuberculosis* (strain H37Rv)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70667
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70667
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-129 <COL>
A:Cross-references: UNIPROT:P95144; GB:Z83859; GB:AL123456; NID:G3261678; PIDN:CAB06142.
A:Experimental source: strain H37Rv
C:Genetics:

A:Gene: RV1871c

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 32
B84295
hypothetical protein Vng1407c [imported] - *Halobacterium* sp. NRC-1
C:Species: *Halobacterium* sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004
C:Accession: B84295
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A>Title: Genome sequence of *Halobacterium* species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <STO>
A:Cross-references: UNIPROT:Q9HPZ1; GB:AE004437; NID:G10580910; PIDN:AAG19726.1; GSPDB:G
C:Genetics:
A:Gene: VNG1407C
C:Superfamily: thioesterase

Query Match 100.0%; Score 23; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 114 GQPR 117

RESULT 33
H84961
hypothetical protein [imported] - *Buchnera* sp. (strain APS)
C:Species: *Buchnera* sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: H84961
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. AI
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: H84961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yciA; BU274

Query Match 100.0%; Score 23; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 124 GQPR 127

RESULT 34
C72713
hypothetical protein APE1122 - *Aeropyrum pernix* (strain K1)

C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: C72713
 R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: C72713
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <RAW>
 A;Cross-references: UNIPROT:Q9YVC20; DDBJ:AP000060; NID:95104188; PIDN:BAA80107.1; PID:dl
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE1122
 C;Superfamily: Aeropyrum pernix hypothetical protein APE1122

Query Match 100.0%; Score 23; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 109 GQPR 112

RESULT 35
 AB0699
 Probable pathogenicity island effector protein sseE [imported] - Salmonella enterica sub
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0699
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0699
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD01963.1; PID:g16502805; GSPDB:GN00176
 C;Genetics:
 A;Gene: sseE

Query Match 100.0%; Score 23; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 59 GQPR 62

RESULT 36
 T48793
 Hypothetical protein 15E6.10 [imported] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
 C;Accession: T48793
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
 A;Reference number: T24541
 A;Accession: T48793
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <SCH>
 A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.10
 A;Experimental source: cosmid contig 15E6; strain 74

C;Genetics:
 A;Gene: NCSP:15E6.10
 A;Map position: 2
 C;Superfamily: Neurospora crassa hypothetical protein 15E6.10

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 106 GQPR 109

RESULT 37
 T25747
 Hypothetical protein F39B3.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25747
 R;Murray, J.
 submitted to the EMBL Data Library, August 1996
 A;Description: The sequence of C. elegans cosmid F39B3.
 A;Reference number: Z20080
 A;Accession: T25747
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-139 <MUR>
 A;Cross-references: UNIPROT:Q94221; EMBL:U67952; PIDN:AA07576.1; GSPDB:GN00028; CESP:F39B3
 A;Experimental source: strain Bristol N2; clone F39B3
 C;Genetics:
 A;Gene: CESP:F39B3.3
 A;Map position: X

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 38 GQPR 41

RESULT 38
 AH3415
 Hypothetical membrane spanning protein BME11310 [imported] - Brucella melitensis (strain
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C;Accession: AH3415
 R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, P.; Marur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesec Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AH3415
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <KUR>
 A;Cross-references: UNIPROT:Q8YG52; GB:AE008917; PIDN:AAL52491.1; PID:g17983300; GSPDB:GN
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME11310
 A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 21 GQPR 24

```

RESULT 39
I46880
T-cell receptor beta chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46880
R:Komatsu, M.; Lamoyi, E.; Mage, R.G.
J:Immunol. 138, 1621-1626, 1987
A:Title: Genomic DNA encoding rabbit T cell receptor beta-chains: isotypes and allotypes
A:Reference number: I46880; MUID:87110733; PMID:2879869
A:Accession: I46880
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-140 <KOM>
A:Cross-references: GB:M14577; NID:g165715; PIDN:AAA82089.1; PID:g552415
C:Genetics:
A:Gene: TCRB
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match      100.0%; Score 23; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      17 GQPR 20

RESULT 40
E83391
Probable ring-cleaving dioxygenase PA2024 [imported] - Pseudomonas aeruginosa (strain PA
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83391
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <STO>
A:Cross-references: UNIPROT:P23205; GB:AE004629; GB:AE004091; NID:g9948028; PIDN:AA0541
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2024

Query Match      100.0%; Score 23; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      61 GQPR 64

RESULT 41
H75383
Hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75383
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75383
A:Status: preliminary
A:Molecule type: DNA

```

```

A:Residues: 1-141 <WHI>
A:Cross-references: UNIPROT:Q9RU64; GB:AE001997; GB:AE000513; NID:g6459292; PIDN:AAF11102
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1530
A:Map position: 1

Query Match      100.0%; Score 23; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      96 GQPR 99

RESULT 42
E84219
Hypothetical protein Vng0613h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84219
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <STO>
A:Cross-references: UNIPROT:Q9HRN7; GB:AE004437; NID:g10580207; PIDN:AAG19121.1; GSPDB:G
C:Genetics:
A:Gene: VNG0613H

Query Match      100.0%; Score 23; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      106 GQPR 109

RESULT 43
F83267
Conserved hypothetical protein PA3017 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83267
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83267
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <STO>
A:Cross-references: UNIPROT:Q9HZI9; GB:AE004727; GB:AE004091; NID:g9949119; PIDN:AA060640
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3017

Query Match      100.0%; Score 23; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||

```

Db 90 GQPR 93

RESULT 44
S76050
hypothetical protein slr0326 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76050
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Ohta, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76050
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <KAN>
A:Cross-references: UNIPROT:Q55533; EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA1002
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: *Synechocystis* hypothetical protein slr0326

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 37 GQPR 40

RESULT 45
E86741
hypothetical protein yJfi [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86741
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mialme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s.
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: E86741
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <STO>
A:Cross-references: UNIPROT:Q9CH09; GB:AE005176; PID:g12723868; PIDN:AAK05031.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yJfi

Query Match 100.0%; Score 23; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 80 GQPR 83

RESULT 46
S74366
hypothetical protein sll0062 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74366
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Ohta, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74366
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <KAN>
A:Cross-references: UNIPROT:Q55148; EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10284
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 100.0%; Score 23; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 66 GQPR 69

RESULT 47
AE2595
hypothetical protein Atu0155 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2595
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelland, K.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.; Ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <KUR>
A:Cross-references: UNIPROT:Q8UIY6; GB:AE008688; PIDN:AAL41179.1; PID:g17738479; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0155
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 146 GQPR 149

RESULT 48
D70677
hypothetical protein Rv3547 - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70677
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70677
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <COL>
A:Cross-references: UNIPROT:P71854; GB:282098; GB:AL123456; NID:g3261664; PIDN:CAB05059.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3547

Query Match 100.0%; Score 23; DB 2; Length 151;

A:Accession: AF2936
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <KUR>
A:Cross-references: UNIPROT:Q8UBC4; GB:AE008689; PIDN:AAL43508.1; PID:gl17741458; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3092
A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 60 GQPR 63

RESULT 54
E69155
hypothetical protein MTH426 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69155
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69155
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <MTH>
A:Cross-references: UNIPROT:Q26526; GB:AE000827; GB:AE000666; NID:g2621489; PIDN:AAB8493
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH426
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH426

Query Match 100.0%; Score 23; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 55
T46052
ADP-ribosylation factor-like protein T16K5.210 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46052
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23015
A:Accession: T46052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <RIE>
A:Cross-references: UNIPROT:Q9M2X2; EMBL:AL13965
A:Experimental source: cultivar Columbia; BAC clone T16K5
C:Genetics:
A:Map position: 3
A:Introns: 21/3; 32/3; 73/2; 127/2
A>Note: T16K5.210
C:Superfamily: ADP-ribosylation factor
F:110-113/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 54 GQPR 57

RESULT 56
B97639
hypothetical protein AGR_C_4225 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97639
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97639
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: UNIPROT:Q8UD04; GB:AE007869; PIDN:AAK88067.1; PID:gl15157491; GSPDB:B
C:Genetics:
A:Gene: AGR_C_4225
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 62 GQPR 65

RESULT 57
AC2862
ureidoglycolate hydrolase alia [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC2862
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guentbner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: UNIPROT:Q8UD04; GB:AE008688; PIDN:AAL43313.1; PID:gl17740804; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: alia
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 62 GQPR 65

RESULT 58
H86243

hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: H86243
 R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Mafti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H86243
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-166 <STO>
 A:Cross-references: UNIPROT:O23694; GB:AE005172; NID:g2252633; PIDN:AAB65496.1; GSPDB:GN
 C:Genetics:
 A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 77 GQPR 80

RESULT 59
 E75257
 molybdenum cofactor biosynthesis protein C - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
 C:Accession: E75257
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75257
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-168 <WHI>
 A:Cross-references: UNIPROT:Q9RRCL; GB:AE002086; GB:AE000513; NID:g6460395; PIDN:AAF1211
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2571
 A:Map position: 1
 C:Superfamily: Molybdenum cofactor precursor Z biosynthesis protein MoaC

Query Match 100.0%; Score 23; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 17 GQPR 20

RESULT 60
 G95987
 probable ureidoglycolate hydrolase (EC 3.5.3.19) [imported] - Sinorhizobium meliloti (str
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95987
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: G95987
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-170 <KUR>
 A:Cross-references: UNIPROT:Q92UG4; GB:ALS91985; PIDN:CAC49567.1; PID:g15141054; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, L.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Hymann, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: allA; SMD20873
 A:Genome: plasmid
 C:Keywords: hydrolase

Query Match 100.0%; Score 23; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 62 GQPR 65

RESULT 61
 B87593
 hypothetical protein CC2778 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: B87593
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: B87593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <STO>
 A:Cross-references: UNIPROT:Q9A4Q2; GB:AE005673; NID:g13424376; PIDN:AAK24742.1; GSPDB:G
 C:Genetics:
 A:Gene: CC2778

Query Match 100.0%; Score 23; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 152 GQPR 155

RESULT 62
 T50632
 hypothetical protein DKFZp762E1511.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C:Accession: T50632
 R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
 submitted to the Protein Sequence Database, June 2000
 A:Reference number: Z25145
 A:Accession: T50632
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-171 <AAA>
 A:Cross-references: UNIPROT:Q9NPV6; EMBL:AL359614

A:Experimental source: adult melanoma (MeWo cell line); clone DKF2p762E1511
 C:Genetics:
 A:Note: DKF2p762E1511.1

Query Match 100.0%; Score 23; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 26 GQPR 29

RESULT 63

B75494

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: B75494

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: B75494

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <WHI>

A:Cross-references: UNIPROT:Q9RWL3; GB:AE001922; GB:AE000513; NID:g6458343; PIDN:AAF1022

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0653

A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 128 GQPR 131

RESULT 64

F83819

hypothetical protein BH1358 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: F83819

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83819

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <STO>

A:Cross-references: UNIPROT:Q9KDG1; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB050

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1358

Query Match 100.0%; Score 23; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 162 GQPR 165

RESULT 65

T08126

pathogenesis-related protein 1 precursor - pepper

C:Species: Capsicum annuum (pepper)

C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C:Accession: T08126

R:Wang, B.K.; Kim, Y.J.

submitted to the EMBL Data Library, March 1998

A:Description: Molecular cloning and pathogen, ethylene and developmental dependent exper

A:Reference number: Z16370

A:Accession: T08126

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-177 <HWA>

A:Cross-references: UNIPROT:O65157; EMBL:AF053343; NID:g2981170; PIDN:AAC06244.1; PID:g29

A:Experimental source: cultivar Hanbyul

C:Superfamily: pathogenesis-related leaf protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-177/Product: pathogenesis-related protein 1 #status predicted <MAT>

Query Match 100.0%; Score 23; DB 2; Length 177;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 154 GQPR 157

RESULT 66

T19610

hypothetical protein C31E10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19610

R:Swinburne, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19151

A:Accession: T19610

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-177 <WIL>

A:Cross-references: UNIPROT:Q93311; EMBL:Z78539; PIDN:CAB01728.1; GSPDB:GN000028; CESP:C31

A:Experimental source: clone C31E10

C:Genetics:

A:Gene: CESP:C31E10.2

A:Map position: X

A:introns: 18/1

Query Match 100.0%; Score 23; DB 2; Length 177;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 78 GQPR 81

RESULT 67

H87430

flagellin modification protein, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: H87430

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

N, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: H87430

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <STO>

A;Cross-references: UNIPROT:Q9A897; GB:AE005673; NID:g13422832; PIDN:AAK23444.1; GSPDB:G
 C;Genetics:
 A;Gene: CCL464

Query Match 100.0%; Score 23; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 150 GQPR 153

RESULT 68
 T27225

ADP-ribosylation factor Y57G11C.13 [similarity] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T27225

R;McMurray, A.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z20330
 A;Accession: T27225
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-185 <WIL>
 A;Cross-references: UNIPROT:Q18237; EMBL:Z39281; PIDN:CAB16514.1; GSPDB:GN000022; CESP:Y5
 A;Experimental source: clone Y57G11C
 C;Genetics:
 A;Gene: CESP:Y57G11C.13
 A;Map position: 4
 A;Introns: 41/3; 171/1
 C;Superfamily: ADP-ribosylation factor
 F;130-133/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 74 GQPR 77

RESULT 69
 T34807

probable transcription regulator - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C;Accession: T34807

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1998
 A;Reference number: Z21557
 A;Accession: T34807
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-185 <MUR>
 A;Cross-references: UNIPROT:Q69909; EMBL:AL023797; PIDN:CAA19414.1; GSPDB:GN000070; SCOE
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOE:SC2E1.39

Query Match 100.0%; Score 23; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 140 GQPR 143

RESULT 70
 B82649

ADP-ribosylation factor Y57G11C.13 [similarity] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T27225

R;McMurray, A.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z20330
 A;Accession: T27225
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-185 <WIL>
 A;Cross-references: UNIPROT:Q18237; EMBL:Z39281; PIDN:CAB16514.1; GSPDB:GN000022; CESP:Y5
 A;Experimental source: clone Y57G11C
 C;Genetics:
 A;Gene: CESP:Y57G11C.13
 A;Map position: 4
 A;Introns: 41/3; 171/1
 C;Superfamily: ADP-ribosylation factor
 F;130-133/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 13 GQPR 16

RESULT 71
 T46053

ADP-ribosylation factor-like protein T16K5.220 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, F.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23015
 A;Accession: T46053
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-190 <RIE>
 A;Cross-references: UNIPROT:Q9M2X1; EMBL:AL132965
 A;Experimental source: cultivar Columbia; BAC clone T16K5
 C;Genetics:
 A;Map position: 3
 A;Introns: 21/3; 71/2
 A;Note: T16K5.220
 C;Superfamily: ADP-ribosylation factor
 F;108-111/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 52 GQPR 55

RESULT 72

hypothetical protein XF1705 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: B82649

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: B82649
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-186 <SIM>
 A;Cross-references: UNIPROT:Q9PCS3; GB:AE003994; GB:AE003849; NID:g9106756; PIDN:AAF84514
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.;
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Experimental source:
 C;Contents: annotation
 C;Genetics:
 A;Gene: XF1705

Query Match 100.0%; Score 23; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 13 GQPR 16

RESULT 71
 T46053

ADP-ribosylation factor-like protein T16K5.220 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, F.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23015
 A;Accession: T46053
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-190 <RIE>
 A;Cross-references: UNIPROT:Q9M2X1; EMBL:AL132965
 A;Experimental source: cultivar Columbia; BAC clone T16K5
 C;Genetics:
 A;Map position: 3
 A;Introns: 21/3; 71/2
 A;Note: T16K5.220
 C;Superfamily: ADP-ribosylation factor
 F;108-111/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 52 GQPR 55

RESULT 72

A75518
guanyl-specific ribonuclease SA - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75518
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75518
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <WHO>
A:Cross-references: UNIPROT:Q9RX62; GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF1002
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0453
A:Map position: 1
C:Superfamily: ribonuclease Sa

Query Match 100.0%; Score 23; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 60 GQPR 63

RESULT 73
A83008
conserved hypothetical protein PA5104 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83008
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83008
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <STO>
A:Cross-references: UNIPROT:Q9HU79; GB:AE004923; GB:AE004091; NID:g9951395; PIDN:AAG0848
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5104
C:Superfamily: Yersinia pestis hypothetical protein PL09040.8

Query Match 100.0%; Score 23; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 155 GQPR 158

RESULT 74
H87446
potassium-transporting ATPase, C subunit CC1593 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 27-Oct-2003
C:Accession: H87446
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n, J.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87446
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:AE005673; NID:g13422988; PIDN:AAK33572.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1593
C:Superfamily: H+/K+-exchanging ATPase subunit C

Query Match 100.0%; Score 23; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 171 GQPR 174

RESULT 75
B96902
probable NADPH-quinone reductase, YabF family [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B96902
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B96902
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <KUR>
A:Cross-references: UNIPROT:Q97N20; GB:AE001437; PIDN:AAK78005.1; PID:g15022837; GSPDB:G
C:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0018

Query Match 100.0%; Score 23; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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Db 112 GQPR 115

Search completed: May 17, 2005, 10:06:57
Job time : 35 secs

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